

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 29, 2006, 13:42:19 ; Search time 41 Seconds
(without alignments)
877.685 Million cell updates/sec

Title: US-10-791-592-2
Perfect score: 1970
Sequence: 1 MLSTSRFRFRNTNESGEV.....GKGSGTGRAPEASLDQKEGA 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283415

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 99.9999%
Listing first 1045 summaries

Database : PIR_80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1651.5	83.8	360	2 JC2443	chemokine (C-C) re
2	1224	62.1	352	2 A43113	chemokine (C-C) re
3	967.5	49.1	355	2 A45177	chemokine (C-C) re
4	960	48.7	359	2 I49341	MIP-1 alpha recept
5	902.5	45.8	355	2 I49339	macrophage inflam
6	890.5	45.2	355	2 G02436	chemokine (C-C) re
7	833	42.3	360	2 JC4587	chemokine (C-C) re
8	831.5	42.2	360	2 A57160	chemokine (C-C) re
9	794.5	40.3	383	2 S55594	G protein-coupled
10	731	37.1	356	2 I49340	MIP-1 alpha recept
11	723	36.7	355	2 JC5067	G protein-coupled
12	704.5	35.8	354	2 I58186	probable G protein
13	698	35.4	355	2 JC4304	orphan G protein-c
14	644.5	32.7	344	2 JC5942	chemokine receptor
15	584	29.6	378	2 B55735	lymphocyte-specifi
16	575.5	29.2	378	2 A55735	G protein-coupled
17	570	28.9	378	2 A45680	G protein-coupled
18	554.5	28.1	369	2 A53068	G protein-coupled
19	541.5	27.5	360	2 A53611	interleukin-8 rece
20	537	27.3	359	2 A48921	interleukin-8 rece
21	531	27.0	352	2 G00048	fusin (LSTR) - c
22	530.5	26.9	353	2 S28787	neuropeptide Y/pep
23	529.5	26.9	355	2 JC1231	interleukin-8 rece
24	528	26.8	352	2 A45747	neuropeptide Y/pep
25	526	26.7	358	2 A53752	interleukin-8 rece
26	526	26.7	367	2 JB0349	interferon-inducib
27	524.5	26.6	350	2 A39445	interleukin-8 rece
28	523	26.5	356	2 S42086	interleukin-8 rece
29	519	26.3	333	2 I65989	G protein-coupled

30	484	24.6	350	2 JN0621	G protein-coupled
31	480	24.4	359	2 A42656	angiotensin II rec
32	479.5	24.3	359	2 S42628	G protein-coupled
33	475	24.1	359	2 I51372	angiotensin II rec
34	473	24.0	359	2 JC2134	angiotensin II rec
35	472	24.0	359	2 JH0621	angiotensin II rec
36	471	23.9	359	2 S15403	angiotensin II rec
37	471	23.9	359	2 JQ1516	angiotensin II rec
38	469	23.8	359	2 JC1104	angiotensin II rec
39	468	23.8	359	2 S44425	angiotensin II rec
40	465	23.6	359	2 JC1194	angiotensin II rec
41	465	23.6	374	2 S32785	G protein-coupled
42	464	23.6	359	2 A48857	angiotensin II rec
43	461.5	23.4	372	2 S26667	G protein-coupled
44	460.5	23.4	327	2 S56162	MCCR15 protein - h
45	456	23.1	354	2 T09353	G protein-coupled
46	456	23.1	359	2 I39418	angiotensin II rec
47	450	22.8	323	1 Q08BD3	HRF3 protein - hu
48	449.5	22.8	363	2 I48261	angiotensin II rec
49	442.5	22.5	363	2 A49092	angiotensin II rec
50	438.5	22.3	363	2 JC2543	angiotensin II rec
51	433.5	22.0	362	2 JN0694	angiotensin II rec
52	425	21.6	354	2 A23669	interleukin-8 rece
53	413	21.0	362	2 A30341	G protein-coupled
54	410	20.8	362	2 A39714	G protein-coupled
55	409	20.8	380	2 A48227	kappa opioid recep
56	408	20.7	380	2 S36143	kappa opioid recep
57	407	20.7	380	2 A55259	kappa opioid recep
58	406	20.6	380	2 JC2338	kappa opioid recep
59	405	20.6	380	2 JC2434	kappa opioid recep
60	395.5	20.1	388	2 JN0605	somatostatin recep
61	392.5	19.9	384	2 A47449	brain-specific som
62	392	19.9	354	2 B55733	G protein-coupled
63	386.5	19.6	384	2 JC4629	somatostatin recep
64	381.5	19.4	364	2 JQ1488	bradykinin B2 rece
65	380.5	19.3	308	2 I50241	G protein-coupled
66	373.5	19.0	367	2 JC2421	opioid receptor ho
67	373.5	19.0	367	2 I49022	kappa opioid recep
68	373.5	19.0	367	2 I56520	G protein-coupled
69	373	18.9	363	2 I57955	somatostatin recep
70	373	18.9	364	2 JN0763	somatostatin recep
71	373	18.9	370	2 S43087	orphan opioid rece
72	372	18.9	366	2 I49519	bradykinin B2 rece
73	370.5	18.8	344	2 T09508	intronic 17 puriner
74	369.5	18.8	372	2 S34592	delta opioid recep
75	369	18.7	333	2 I38974	G protein-coupled
76	368.5	18.7	398	2 A57510	mu opioid receptor
77	368	18.7	366	1 O0RTB2	bradykinin recepto
78	367.5	18.7	380	2 I38435	angiotensin recept
79	365.5	18.6	398	2 I56504	mu opioid receptor
80	365	18.5	392	2 S65693	opioid receptor mu
81	363.5	18.5	398	2 I56517	mu opioid receptor
82	363	18.4	391	2 A41795	somatostatin recep
83	363	18.4	391	2 C41795	somatostatin recep
84	363	18.4	391	2 A39297	somatostatin recep
85	362.5	18.4	372	2 I38532	delta opioid recep
86	362.5	18.4	400	2 I56553	mu opiate receptor
87	362	18.4	352	2 S60024	bradykinin B1 rece
88	359.5	18.2	371	2 JC5498	G protein-coupled
89	359.5	18.2	418	2 A46226	somatostatin recep
90	358.5	18.2	372	2 B48227	delta opioid recep
91	357	18.1	363	2 I57940	somatostatin recep
92	356	18.1	353	2 A53858	bradykinin recepto
93	355	18.0	364	2 A49542	N-formyl peptide c
94	355	18.0	371	2 JC5796	probable chemoattr
95	355	18.0	373	2 JH0087	delta opioid recep
96	346.5	17.6	423	2 JC7677	allatostatin recep
97	345.5	17.5	361	2 B45680	G protein-coupled
98	345	17.5	420	2 I51667	thrombin receptor
99	343.5	17.4	369	2 JC2083	somatostatin recep
100	341	17.3	369	2 D41795	somatostatin recep
101	339	17.2	346	2 S29248	somatostatin recep
102	339	17.2	357	2 JC7319	probable allatosta

103	339	17.2	428	2	S30508	probable G protein	176	268.5	13.6	519	2	S17783	tachykinin recepto
104	338.5	17.2	428	2	A44021	somatostatin recep	177	267.5	13.6	455	2	T15622	hypothetical prote
105	338	17.2	369	2	B41795	somatostatin recep	178	266	13.5	436	2	JC5599	cholecystokinin-A
106	338	17.2	369	2	A45291	somatostatin recep	179	265.5	13.5	384	2	A41007	gasirin-releasing
107	334	17.0	394	2	JC7209	galanin receptor -	180	265.5	13.5	384	2	I57682	bombesin/ GRP rece
108	332.5	16.9	370	2	JC5549	heptahelical P2Y5-	181	265	13.5	457	2	T29741	hypothetical prote
109	328	16.6	373	2	JC4737	G protein-coupled	182	263.5	13.4	399	2	A46632	bombesin-like pept
110	327.5	16.6	328	2	I38973	G protein-coupled	183	262.5	13.3	328	2	JC4800	P2Y6 receptor - hu
111	326.5	16.6	351	2	B42009	FMPL-related recep	184	262.5	13.3	340	2	JC7695	G protein-coupled
112	325.5	16.5	355	2	A55733	G protein-coupled	185	262.5	13.3	390	2	A36737	neurokinin 2 recep
113	325	16.5	399	2	I48705	proteinase activat	186	261	13.2	440	2	A44081	kappa-type opioid
114	324.5	16.5	353	2	JC2492	G protein-coupled	187	260.5	13.2	349	2	S12863	G protein-coupled
115	324.5	16.5	427	2	S17148	alpha-thrombin rec	188	260.5	13.2	382	2	B46133	neuropeptide Y/pep
116	324	16.4	373	2	JC4162	P2Y receptor - bov	189	260.5	13.2	382	2	S27388	neuropeptide Y recep
117	322.5	16.4	342	2	S13638	platelet-activatin	190	260	13.2	385	2	S55524	neurokinin 3 recep
118	321	16.3	334	2	JC4681	bradykinin B1 rece	191	260	13.2	465	1	JQ1517	neurokinin 2 recep
119	320.5	16.3	350	2	A42009	N-formyl peptide r	192	258.5	13.1	384	2	I57957	neurokinin 3 recep
120	317	16.1	362	2	S33733	G protein-coupled	193	258.5	13.1	384	2	S20303	neurokinin 2 recep
121	315.5	16.0	359	2	JC5277	G protein-coupled	194	258	13.1	452	2	A34916	neurokinin 3 recep
122	314.5	16.0	352	1	S27357	complement C5a ana	195	257	13.0	643	2	T19135	cholecystokinin ty
123	314	15.9	360	2	G02064	G protein-coupled	196	256.5	13.0	366	2	S71152	neuropeptide Y/pep
124	312.5	15.9	342	2	A40191	platelet-activatin	197	255.5	13.0	412	2	T22076	hypothetical prote
125	312	15.8	351	2	JC7096	leukotriene B4 rec	198	255	12.9	359	2	JC4120	histamine H2 recep
126	309	15.7	350	1	A37963	complement C5a ana	199	255	12.9	477	2	JC7913	capa receptor (CGI
127	308	15.6	387	2	JC5949	galanin receptor 2	200	254.5	12.9	366	2	I46469	Mel-1a melatonin r
128	307.5	15.6	397	2	S66518	proteinase-activat	201	254.5	12.9	373	2	A47556	Mel-1c receptor su
129	306.5	15.6	352	2	A46520	N-formyl peptide r	202	254.5	12.9	420	2	I51666	HHR23 protein - hu
130	305	15.5	449	2	A41738	neuropeptide Y rec	203	254	12.9	362	1	Q0BED2	endothelin recepto
131	304.5	15.5	422	2	JC7080	melanin-concentrat	204	254	12.9	441	2	S13425	nonselective-type
132	304	15.4	351	1	A46525	complement C5a ana	205	253.5	12.9	442	2	I57950	bombesin receptor
133	303	15.4	352	2	JE0296	thyrotropin releas	206	253	12.8	399	2	S29480	glucocorticoid-ind
134	302	15.3	432	2	A43448	thrombin receptor	207	253	12.8	491	2	C40470	vasotocin receptor
135	301.5	15.3	375	2	SJ0569	G protein-coupled	208	252.5	12.8	434	2	I50132	angiotensin II rec
136	301	15.3	365	2	S68679	G protein-coupled	209	252	12.8	177	2	PH1372	G protein-coupled
137	300	15.2	341	2	S63666	platelet activatin	210	252	12.8	482	2	S65766	hypothetical prote
138	300	15.2	430	2	I51898	cholecystokinin A	211	251.5	12.8	539	2	T27559	histamine H2 recep
139	298.5	15.2	390	2	JH0374	bombesin receptor,	212	250	12.7	359	2	A39008	Phel3 bombesin rec
140	296	15.0	341	2	S43252	platelet-activatin	213	249.5	12.7	376	2	I50102	hypothetical prote
141	295	15.0	423	2	B40470	glucocorticoid-ind	214	248.5	12.6	365	2	T20184	G protein-coupled
142	294.5	14.9	349	2	I59236	galanin receptor 1	215	248.5	12.6	370	1	I52315	G protein-coupled
143	294.5	14.9	375	2	JC5509	G protein-coupled	216	247	12.5	580	2	H87963	protein Y54E2A.1 l
144	294	14.9	411	2	I56444	thyrotrophin-relea	217	247	12.5	658	2	JC8011	G protein-coupled
145	294	14.9	412	2	S23436	thyroliberin recep	218	244.5	12.4	359	2	JH0449	histamine H2 recep
146	292.5	14.8	365	2	S68208	G protein-coupled	219	244.5	12.4	447	2	A47430	gasirin/cholecycto
147	289.5	14.7	398	2	JN0708	thyrotropin-releas	220	243	12.3	381	2	A40470	glucocorticoid-ind
148	289	14.7	444	2	T27866	hypothetical prote	221	241	12.2	375	2	A54946	P-2U nucleotide re
149	286.5	14.5	395	2	S40685	probable G protein	222	241	12.2	376	2	T19186	hypothetical prote
150	285.5	14.5	387	2	I69202	G protein-coupled	223	240.5	12.2	381	2	T29300	hypothetical prote
151	284.5	14.4	328	2	I55450	G protein-coupled	224	239.5	12.2	477	2	S71323	alpha-1A adrenergi
152	283.5	14.4	390	2	B41007	bombesin receptor,	225	239	12.1	407	1	JQ1274	neurokinin 1 recep
153	283.5	14.4	428	2	JN0692	cholecystokinin ty	226	238.5	12.1	504	2	A41783	tachykinin recepto
154	283	14.4	584	2	JC7809	sulfakinin recepto	227	238	12.1	407	2	S20304	neurokinin 1 recep
155	282	14.3	393	2	A39251	thyrotropin-releas	228	237.5	12.1	374	2	T19340	hypothetical prote
156	282	14.3	362	2	B57641	G protein-coupled	229	237.5	12.1	391	2	T32517	hypothetical prote
157	281	14.3	404	2	JC5784	adrenomedullin rec	230	237	12.0	351	1	A55962	opsin, pineal glan
158	281	14.3	444	2	A42685	cholecystokinin re	231	237	12.0	407	2	S43357	neurokinin 1 recep
159	280.5	14.2	425	2	A37912	thrombin receptor	232	236	12.0	418	2	S29506	neurotensin recept
160	280	14.2	354	2	I53033	G protein-coupled	233	235.5	12.0	350	2	I38848	Mel-1a melatonin r
161	280	14.2	362	2	A57641	G protein-coupled	234	234.5	11.9	595	2	JC8012	G protein-coupled
162	278	14.1	362	2	S68207	G protein-coupled	235	233	11.8	386	2	I84612	sensory epithelia
163	277.5	14.1	353	2	C42009	FMPL-related recep	236	233	11.8	407	2	S23510	GnHR receptor homo
164	277	14.1	384	1	S00516	neurokinin 2 recep	237	232	11.8	443	2	JC2459	gasirin/cholecycto
165	277	14.1	402	2	I56595	neurokinin 2 recep	238	232	11.8	452	2	JC2459	anaphylatoxin C3a
166	276	14.0	358	2	G02670	neurokinin 2 recep	239	232	11.8	473	2	JC5835	endothelin recepto
167	275	14.0	443	2	D40470	glucocorticoid-ind	240	231.5	11.8	442	1	JQ1042	endothelin recepto
168	274.5	13.9	613	2	S70520	melatonin receptor	241	230.5	11.7	441	2	A41591	protein UL33 - hum
169	274	13.9	398	1	JQ1059	neurokinin 2 recep	242	230	11.7	390	1	Q0BET9	neurotensin recept
170	274	13.9	427	2	S50150	gastric CCK-A rece	243	230	11.7	424	2	JH0164	neurotensin recept
171	273	13.9	361	2	JC5653	G protein-coupled	244	230	11.7	450	2	JQ1614	gasirin receptor -
172	270.5	13.7	328	2	T30999	hypothetical prote	245	229	11.6	452	2	A46195	cholecystokinin B
173	270	13.7	384	2	A45490	neuropeptide Y/pep	246	228.5	11.6	375	2	S63685	neuropeptide Y rec
174	270	13.7	391	2	T32714	hypothetical prote	247	228	11.6	448	1	S29483	rhodopsin [similar
175	268.5	13.6	384	2	A39003	bombesin/gastrin-r	248	228	11.6	477	2	T25846	hypothetical prote

KAG

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 29, 2006, 13:38:04 ; Search time 188 Seconds
(without alignments)
874.083 Million cell updates/sec

Title: us-10-791-592-2
Perfect score: 1970
Sequence: 1 MLSTSRFRFIRNTNSESREV.....GKGKSTORAPASLQDKEGA 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443149

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 99.9999%
Listing first 1045 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1823	92.5	344	5	ABG92881 Class I r
2	1823	92.5	344	6	ABU61655 Human mon
3	1823	92.5	344	7	ADP72129 Human G-p
4	1823	92.5	344	8	ADP86217 Human MCP
5	1727.5	87.7	329	4	AB46859 Human MCP
6	1727.5	87.7	329	5	ABH81055 Human MCP
7	1727.5	87.7	329	8	ADP79166 Human mon
8	1651.5	83.8	360	2	AAW35833 Human mon
9	1651.5	83.8	360	2	AAW35833 Human mon
10	1651.5	83.8	360	4	AAW35833 Human mon
11	1651.5	83.8	360	4	AAW35833 Human mon
12	1651.5	83.8	360	6	AAW35833 Human mon
13	1651.5	83.8	360	6	AAW35833 Human mon
14	1651.5	83.8	360	8	ADL82831 Human PRO
15	1651.5	83.8	360	8	ADL82831 Human PRO
16	1651.5	83.8	360	9	ADY15868 Human CCR
17	1650.5	83.8	360	4	AAU07613 Human CCR
18	1645.5	83.5	360	4	ABBS6340 Non-endo
19	1589.5	80.7	347	7	ADP56627 Partial h
20	1589.5	80.7	347	9	ADW15156 Human mon
21	1582.5	80.3	384	9	AE22130 Human che
22	1332.5	67.6	373	8	ADM67224 Murine ad
23	1332.5	67.6	373	8	ADO29222 Mouse GPC
24	1332.5	67.6	373	8	ADP74040 Murine CC

25	1244	63.1	354	8	ADO29228	Mouse GPC
26	1236	62.7	352	4	AAW9089	Amino aci
27	1234	62.6	354	4	AAW54037	Mouse CC-
28	1230	62.4	354	7	ADD44859	Rat Prote
29	1230	62.4	354	7	ADD44863	Rat Prote
30	1224	62.1	352	2	AAW27407	Human CCR
31	1224	62.1	352	2	AAW27123	Human che
32	1224	62.1	352	2	AAW27125	Macaque c
33	1224	62.1	352	2	AAW23835	Human CC
34	1224	62.1	352	2	AAW88232	HIV-1 co-
35	1224	62.1	352	4	AAE07048	Human CCR
36	1224	62.1	352	4	AAE07048	Human CCR
37	1224	62.1	352	4	AAE04321	Human che
38	1224	62.1	352	4	AAE07039	Human G-p
39	1224	62.1	352	4	AAW46858	Human HDG
40	1224	62.1	352	4	AAW83354	Human CCR
41	1224	62.1	352	4	AAW82948	Human HIV
42	1224	62.1	352	5	AAU97152	Human G-p
43	1224	62.1	352	5	AAW52828	Human CC
44	1224	62.1	352	5	ABG70597	Human G-p
45	1224	62.1	352	5	ABG92883	Human imm
46	1224	62.1	352	5	AAE25811	Human G-p
47	1224	62.1	352	5	ABW81054	G-protein
48	1224	62.1	352	5	ABW81054	G-protein
49	1224	62.1	352	6	ABG75540	Human G-p
50	1224	62.1	352	6	ABR58602	Human can
51	1224	62.1	352	6	AAO29514	Human C-C
52	1224	62.1	352	6	ABU61654	Human G-p
53	1224	62.1	352	6	ABP97728	Amino aci
54	1224	62.1	352	6	ABP81933	Human C-C
55	1224	62.1	352	7	ADC03341	Human che
56	1224	62.1	352	7	ADC03359	Macaque c
57	1224	62.1	352	7	ADF72142	Human G-p
58	1224	62.1	352	7	ADF44882	Human CC
59	1224	62.1	352	7	ADK17356	Human CCR
60	1224	62.1	352	7	ADP65192	Human che
61	1224	62.1	352	8	ADG42778	Human CC
62	1224	62.1	352	8	ADM60807	Human CC-
63	1224	62.1	352	8	ADM35887	Human che
64	1224	62.1	352	8	ADO29227	Human GPC
65	1224	62.1	352	8	ADP12403	Protein e
66	1224	62.1	352	8	ADP19578	Human PRO
67	1224	62.1	352	8	ADP86210	Human G-p
68	1224	62.1	352	8	ADQ21275	Human sof
69	1224	62.1	352	8	ADP16259	Human G-p
70	1224	62.1	352	8	ADP24004	PRO poly
71	1224	62.1	352	8	ADT90865	Macaque s
72	1224	62.1	352	8	ADT90847	Human che
73	1224	62.1	352	8	ADU47744	Macaque c
74	1224	62.1	352	8	ADU47726	Human che
75	1224	62.1	352	9	ADY19490	PRO poly
76	1224	62.1	352	9	ADY15766	PRO poly
77	1224	62.1	352	9	ADY15766	PRO poly
78	1224	62.1	352	9	ADY15766	PRO poly
79	1219.5	61.9	371	2	AAW41280	Fusion pr
80	1218	61.8	352	4	ABBS6342	Non-endo
81	1218	61.8	352	5	AAW52829	Human CCR
82	1215	61.7	352	3	AAW07602	Human G-p
83	1215	61.7	352	3	AAW80128	Human G-p
84	1215	61.7	352	4	AAE07046	Human G-p
85	1215	61.7	352	4	AAE07037	Human G-p
86	1215	61.7	352	5	AAU97150	Human G-p
87	1215	61.7	352	5	ABG92880	Human G-p
88	1215	61.7	352	5	AAE25808	Human G-p
89	1215	61.7	352	7	ADP72122	Human G-p
90	1204.5	61.1	326	8	ADY27192	Amino aci
91	1200	60.9	300	8	ADY27202	Amino aci
92	1195.5	60.7	332	2	AAW26766	Human che
93	967.5	49.1	355	2	AAW52749	C-C Chemo
94	967.5	49.1	355	2	AAW25751	Human MIP
95	967.5	49.1	355	2	AAW26588	Human MIP
96	967.5	49.1	355	3	AAW20571	Human CC-
97	967.5	49.1	355	3	ADZ28066	Human CC-

98	967.5	49.1	355	4	AAG80106	Aag80106 Human CCR	171	831.5	42.2	360	9	ADY20385	Ady20385 PRO polyp
99	967.5	49.1	355	5	ADZ58688	Adz58688 Human CCR	172	831.5	42.2	360	9	ADZ11715	Adz11715 Human che
100	967.5	49.1	355	6	ABU09082	Abu09082 Human che	173	831.5	42.2	360	9	ADZ52555	Adz52555 Human CC
101	967.5	49.1	355	6	ABP97724	Abp97724 Amino aci	174	831.5	42.2	360	9	AEA33220	Aea33220 Human CC
102	967.5	49.1	355	6	ABP81790	Abp81790 Human C-C	175	831.5	42.2	361	4	ABB11966	Abb11966 Human CCR
103	967.5	49.1	355	7	ADF76506	Adf76506 Novel hum	176	828.5	42.1	360	2	AAR99274	Aar99274 Chemokine
104	967.5	49.1	355	7	ADO16838	Ado16838 CCR1 amin	177	828.5	42.1	360	6	ABP97727	Abp97727 Amino aci
105	967.5	49.1	355	8	ADO29219	Ado29219 Human GPC	178	794.5	40.3	383	6	ABP81684	Abp81684 G protein
106	967.5	49.1	355	8	ADO19490	Ado19490 Human PRO	179	731	37.1	356	5	AAC22920	Aac22920 356 aa G-
107	967.5	49.1	355	8	ADO19492	Ado19492 Human PRO	180	731	37.1	356	5	ADO29711	Ado29711 Mouse GPC
108	967.5	49.1	355	8	ADQ21524	Adq21524 Human sof	181	730	37.1	355	5	AU80223	Au80223 Human Che
109	967.5	49.1	355	8	ADP88568	Adp88568 Human che	182	723	36.7	355	2	AAW07618	Aaw07618 Human G-p
110	967.5	49.1	355	8	ADP88570	Adp88570 Human mac	183	723	36.7	355	2	AAW49807	Aaw49807 Human G-p
111	967.5	49.1	355	8	ADQ67846	Adq67846 Human che	184	723	36.7	355	4	AAW97868	Aaw97868 Human CC
112	967.5	49.1	355	8	ADR14581	Adr14581 Human NF-	185	723	36.7	355	4	AAG80115	Aag80115 Human CCR
113	967.5	49.1	355	9	ADY15488	Ady15488 PRO polyp	186	723	36.7	355	5	AU80222	Au80222 Human Che
114	967.5	49.1	355	9	ADY19562	Ady19562 PRO polyp	187	723	36.7	355	5	AU77932	Au77932 Human G-p
115	967.5	49.1	355	9	ADY15486	Ady15486 PRO polyp	188	723	36.7	355	6	ABP97731	Abp97731 Amino aci
116	967.5	49.1	355	9	ADZ11712	Adz11712 Human che	189	723	36.7	355	6	ABP81794	Abp81794 Human C-C
117	967.5	49.1	355	9	AEA23748	Aea23748 Human PRO	190	723	36.7	355	7	ADF56626	Adf56626 Human G-p
118	967.5	49.1	355	9	AEA23621	Aea23621 Human PRO	191	723	36.7	355	8	ADF30384	Adf30384 Human che
119	967.5	49.1	355	9	ABE22127	Aeb22127 Human che	192	723	36.7	355	8	ADO43139	Ado43139 Human che
120	951.5	48.3	359	8	ADO29224	Ado29224 Mouse GPC	193	723	36.7	355	8	ADO29233	Ado29233 Human GPC
121	920.5	46.7	355	2	AAW29179	Aaw29179 Rat CC ch	194	723	36.7	355	9	ADW15155	Adw15155 Human HGB
122	920.5	46.7	355	2	ADD45360	Add45360 Rat Prote	195	723	36.7	358	5	AAU77933	Aau77933 Human G-p
123	899.5	45.7	355	5	ADZ58687	Adz58687 Mouse CCR	196	718	36.4	355	4	ABB56343	Abb56343 Non-endo
124	899.5	45.7	355	5	ADO29220	Ado29220 Mouse GPC	197	717	36.4	355	2	AAW56689	Aaw56689 Human MCP
125	899.5	45.7	355	8	ADS86071	Ads86071 Mouse ato	198	708.5	36.0	353	8	ADO29234	Ado29234 Mouse GPC
126	898.5	45.6	379	9	ABE22128	Aeb22128 Human che	199	704.5	35.8	354	8	ADH10684	Adh10684 Rat Sprag
127	897.5	45.6	355	2	AAW51744	Aaw51744 Human C-C	200	698	35.4	355	2	AAW53748	Aaw53748 Seven tra
128	890.5	45.2	355	2	AAW03376	Aaw03376 CC-chemok	201	698	35.4	355	2	AAW48722	Aaw48722 Human V28
129	890.5	45.2	355	2	AAW10100	Aaw10100 Human C-C	202	698	35.4	355	3	AAY90642	Aay90642 Human G-p
130	890.5	45.2	355	5	ABB07240	Abb07240 Human CC	203	698	35.4	355	3	ABZ21693	Abz21693 Human 7TM
131	890.5	45.2	355	5	ABB07733	Abb07733 Human C-C	204	698	35.4	355	3	ABZ21692	Abz21692 Human 7TM
132	890.5	45.2	355	6	ABG72634	Abg72634 Human C-C	205	698	35.4	355	4	AAG80126	Aag80126 Human CX3
133	886.5	45.0	332	5	ABJ03698	Abj03698 Human ova	206	698	35.4	355	4	AAB82786	Aab82786 Human CX3
134	886.5	45.0	355	2	AAW27124	Aaw27124 Human che	207	698	35.4	355	5	AAU91235	Aau91235 Human 7 t
135	886.5	45.0	355	2	AAW31850	Aaw31850 Human eos	208	698	35.4	355	5	AAU84327	Aau84327 Protein C
136	886.5	45.0	355	2	AAW51745	Aaw51745 Human C-C	209	698	35.4	355	6	ABZ58524	Abz58524 Human che
137	886.5	45.0	355	4	AAG80109	Aag80109 Human CCR	210	698	35.4	355	6	ABZ58524	Abz58524 Human fra
138	886.5	45.0	355	4	AAE15320	Aae15320 Human che	211	698	35.4	355	6	ADQ29513	Adq29513 Amino aci
139	886.5	45.0	355	6	ABU09084	Abu09084 Human che	212	698	35.4	355	6	ABP97732	Abp97732 Human CX3
140	886.5	45.0	355	6	ABP97726	Abp97726 Amino aci	213	698	35.4	355	6	ABP81882	Abp81882 Human CX3
141	886.5	45.0	355	6	ABP81791	Abp81791 Human C-C	214	698	35.4	355	7	ADH14122	Adh14122 Human ser
142	886.5	45.0	355	6	ADQ3343	Adq3343 Human che	215	698	35.4	355	7	ADH10680	Adh10680 Human CX3
143	886.5	45.0	355	7	ADO29223	Ado29223 Human GPC	216	698	35.4	355	8	ADO29269	Ado29269 Human GPC
144	886.5	45.0	355	8	ADQ67848	Adq67848 Human che	217	698	35.4	355	8	ADQ18141	Adq18141 Human sof
145	886.5	45.0	355	8	ADT90849	Adt90849 Human che	218	698	35.4	355	8	ADP56020	Adp56020 Human PRO
146	886.5	45.0	355	8	ADU47728	Adu47728 Human che	219	698	35.4	355	8	ADP54585	Adp54585 Human PRO
147	886.5	45.0	355	9	ADY15934	Ady15934 PRO polyp	220	698	35.4	355	8	ADP23931	Adp23931 PRO polyp
148	886.5	45.0	355	9	ADY15934	Ady15934 PRO polyp	221	698	35.4	355	8	ADQ39421	Adq39421 Human myo
149	886.5	45.0	355	9	ADZ11714	Adz11714 Human che	222	698	35.4	355	9	ADY15644	Ady15644 PRO polyp
150	886.5	45.0	355	9	ADZ11714	Adz11714 Human che	223	698	35.4	355	9	ADY15644	Ady15644 PRO polyp
151	881.5	44.7	355	4	ABB56341	Abb56341 Non-endo	224	698	35.4	362	8	ADQ39422	Adq39422 Human myo
152	875	44.4	356	2	AAW25943	Aaw25943 Human CCR	225	694	35.2	184	2	AAW27406	Aaw27406 Inactive
153	875	44.4	356	7	ADC78873	Adc78873 Human PRO	226	694	35.2	188	8	ADM35888	Adm35888 Human CCR
154	867	44.0	355	5	ABB79520	Abb79520 Monkey C-	227	694	35.2	215	2	AAW27408	Aaw27408 Inactive
155	863	43.8	268	7	ADC10144	Adc10144 Human NOV	228	694	35.2	215	2	AAW88238	Aaw88238 HIV-1 co-
156	862.5	43.8	355	2	AAW03378	Aaw03378 CC-chemok	229	693	35.2	255	3	AAV90677	Aav90677 Human mut
157	862.5	43.8	355	2	AAW51746	Aaw51746 Human C-C	230	693	35.2	355	7	ADC22751	Adc22751 Human G-p
158	862	43.8	268	7	ADC10142	Adc10142 Human NOV	231	693	35.2	355	7	ADH14224	Adh14224 Mutated h
159	833	42.2	360	3	ADO29226	Ado29226 Mouse GPC	232	692	35.1	344	9	ADW92148	Adw92148 Mouse CX3
160	831.5	42.2	360	3	AAW07498	Aaw07498 A human C	233	692	35.1	354	8	ADH10682	Adh10682 Mouse CX3
161	831.5	42.2	360	4	AAG80110	Aag80110 Human CCR	234	692	35.1	354	8	ADO29270	Ado29270 Mouse GPC
162	831.5	42.2	360	4	AAG67673	Aag67673 Amino aci	235	688	33.9	164	8	ADM35891	Adm35891 Fusion pr
163	831.5	42.2	360	6	ABR40283	Abra40283 Human ami	236	688	33.9	262	8	ADM35892	Adm35892 Amino aci
164	831.5	42.2	360	6	ABU09085	Abu09085 Human che	237	645.5	32.8	344	2	AAW23957	Aaw23957 Human G-p
165	831.5	42.2	360	6	ABP81792	Abp81792 Human C-C	238	645.5	32.8	344	5	AAU11155	Aau11155 Human G-p
166	831.5	42.2	360	7	ADZ27676	Adz27676 Human seq	239	645.5	32.8	344	5	AAE26111	Aae26111 Human G-p
167	831.5	42.2	360	8	ADO29225	Ado29225 Human GPC	240	645.5	32.8	344	8	ADQ39177	Adq39177 Human myo
168	831.5	42.2	360	8	ADP44057	Adp44057 Human CCR	241	645.5	32.8	344	8	ADQ39178	Adq39178 Human myo
169	831.5	42.2	360	8	ADQ67849	Adq67849 Human che	242	644.5	32.7	344	5	ABB84824	Abb84824 Human PRO
170	831.5	42.2	360	8	ADP56308	Adp56308 Human PRO	243	644.5	32.7	344	5	ABB95430	Abb95430 Human ang

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OM protein - protein search, using sw model

Run on: March 29, 2006, 13:58:15 ; Search time 25 Seconds
(without alignments)
455.411 Million cell updates/sec

Title: US-10-791-592-2

Perfect score: 1970

Sequence: 1 MLSTSRPFRVNTSGEEV.....GKSGSIGRAPEASLDQKGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180807

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

(Maximum Match 99.9999%)

Listing first 1045 summaries

Database : Published Applications AA New.*

- 1: /SIDSS5/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /SIDSS5/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /SIDSS5/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /SIDSS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 5: /SIDSS5/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 6: /SIDSS5/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /SIDSS5/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1224	62.1	352	6	US-10-995-561-523
2	1224	62.1	352	7	US-10-995-561-523
3	1224	62.1	352	7	US-10-995-561-523
4	1224	62.1	352	7	US-10-995-561-523
5	897.5	45.6	355	7	US-11-216-610-2
6	886.5	45.0	355	7	US-11-068-686-4
7	886.5	45.0	355	7	US-11-127-877-64
8	886.5	45.0	355	7	US-11-216-610-4
9	862.5	43.8	355	7	US-11-216-610-6
10	831.5	42.2	360	6	US-10-959-310-36
11	831.5	42.2	360	7	US-11-144-731-1
12	831.5	42.2	360	7	US-11-262-284-34
13	698	35.4	355	6	US-10-995-561-636
14	698	35.4	362	6	US-10-995-561-637
15	696	35.3	216	6	US-10-995-561-522
16	645.5	32.8	344	6	US-10-995-561-524
17	645.5	32.8	344	6	US-10-995-561-525
18	569	28.9	357	7	US-11-261-135-2
19	554.5	28.1	374	7	US-11-127-877-62
20	541.5	27.5	353	7	US-11-017-058-9
21	535	27.1	351	6	US-11-122-849-2
22	534.5	27.1	368	6	US-10-920-055-6
23	534.5	27.1	415	7	US-11-017-058-2
24	528	26.8	352	7	US-11-028-322A-1
25	526	26.7	367	6	US-10-920-055-7

350	7	US-11-249-847-546	Sequence 546, App
349	7	US-11-028-922A-2	Sequence 2, Appl
333	7	US-11-127-877-57	Sequence 57, Appl
348	6	US-10-330-773-921	Sequence 921, App
350	6	US-10-515-604-2	Sequence 2, Appl
359	6	US-10-876-787-2	Sequence 2, Appl
359	6	US-10-995-561-712	Sequence 712, App
359	6	US-10-995-561-716	Sequence 716, App
359	6	US-11-127-877-65	Sequence 65, Appl
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394	6	US-10-995-561-714	Sequence 714, App
394	6	US-10-995-561-715	Sequence 715, App
355	6	US-10-330-773-918	Sequence 918, App
254	6	US-10-055-877-248	Sequence 248, App
254	6	US-10-055-877-327	Sequence 327, App
254	6	US-10-055-877-340	Sequence 340, App
254	6	US-10-877-346-83	Sequence 83, Appl
254	6	US-10-055-877-225	Sequence 225, App
259	6	US-10-055-877-237	Sequence 237, App
259	7	US-11-206-587-27	Sequence 27, Appl
259	7	US-11-206-587-29	Sequence 29, Appl
388	6	US-10-995-561-838	Sequence 838, App
389	6	US-10-995-561-837	Sequence 837, App
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364	7	US-11-040-218-79	Sequence 79, Appl
378	7	US-11-040-218-81	Sequence 81, Appl
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347	7	US-11-040-218-77	Sequence 77, Appl
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400	7	US-11-127-877-55	Sequence 55, Appl
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373	7	US-11-218-281-28	Sequence 28, Appl
337	7	US-11-157-930-5	Sequence 5, Appl
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350	7	US-11-218-281-23	Sequence 23, Appl
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370	6	US-10-330-773-446	Sequence 446, App
352	7	US-11-127-877-59	Sequence 59, Appl
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353	7	US-11-218-281-25	Sequence 25, Appl
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522	6	US-10-510-018-2	Sequence 2, Appl
420	6	US-10-992-577-6	Sequence 6, Appl

99	267	13.6	430	6	US-10-992-577-8	Sequence 8, Appli	172	203	10.3	344	7	US-11-174-819-30	Sequence 30, Appl
100	267	13.6	430	6	US-10-508-892-2	Sequence 2, Appli	173	203	10.3	348	7	US-11-174-751-12	Sequence 12, Appl
101	267	13.6	430	6	US-11-223-294-54	Sequence 54, Appl	174	203	10.3	508	6	US-10-980-388-112	Sequence 112, Appl
102	265.5	13.5	384	7	US-11-127-877-44	Sequence 44, Appl	175	202.5	10.3	349	7	US-11-174-751-22	Sequence 22, Appl
103	262.5	13.3	340	6	US-10-980-388-117	Sequence 117, App	176	202	10.3	477	6	US-10-877-346-47	Sequence 47, Appl
104	261.5	13.3	340	7	US-11-127-877-53	Sequence 53, Appl	177	201.5	10.2	344	7	US-11-174-816-45	Sequence 45, Appl
105	257	13.0	356	7	US-11-218-281-27	Sequence 27, Appl	178	201.5	10.2	344	7	US-11-174-819-28	Sequence 28, Appl
106	252	12.8	482	7	US-11-169-976-2	Sequence 2, Appli	179	200	10.2	381	6	US-10-987-856-16	Sequence 16, Appl
107	252	12.8	482	7	US-11-218-281-30	Sequence 30, Appl	180	199.5	10.1	337	7	US-11-174-816-43	Sequence 43, Appl
108	249.5	12.7	488	7	US-11-206-587-32	Sequence 32, Appl	181	199.5	10.1	337	7	US-11-174-819-11	Sequence 11, Appl
109	248.5	12.6	309	6	US-10-537-002-9	Sequence 9, Appli	182	199.5	10.1	358	7	US-11-174-816-67	Sequence 67, Appl
110	248.5	12.6	394	6	US-10-537-002-10	Sequence 10, Appl	183	199.5	10.1	358	7	US-11-174-819-86	Sequence 86, Appl
111	247.5	12.6	342	7	US-11-151-482-1	Sequence 1, Appli	184	199	10.1	358	7	US-11-174-816-49	Sequence 49, Appl
112	245	12.4	393	7	US-11-073-420-32	Sequence 32, Appl	185	199	10.1	358	7	US-11-174-819-15	Sequence 15, Appl
113	244.5	12.4	393	6	US-10-055-877-179	Sequence 179, App	186	199	10.1	409	6	US-10-627-633-4	Sequence 4, Appli
114	244.5	12.4	412	7	US-11-170-153-8	Sequence 8, Appli	187	199	10.1	456	6	US-10-987-856-2	Sequence 2, Appli
115	244.5	12.4	412	7	US-11-170-166-8	Sequence 8, Appli	188	198.5	10.1	351	7	US-11-174-816-5	Sequence 5, Appli
116	244.5	12.4	412	7	US-11-170-351-8	Sequence 8, Appli	189	198.5	10.1	351	7	US-11-174-819-68	Sequence 68, Appl
117	244.5	12.4	415	7	US-11-170-153-6	Sequence 6, Appli	190	197.5	10.1	358	7	US-11-127-877-66	Sequence 66, Appl
118	244.5	12.4	415	7	US-11-170-166-6	Sequence 6, Appli	191	197.5	10.0	358	6	US-10-055-877-177	Sequence 177, App
119	244.5	12.4	415	7	US-11-170-351-6	Sequence 6, Appli	192	196.5	10.0	337	7	US-11-174-816-58	Sequence 58, Appl
120	243.5	12.4	403	6	US-10-503-511-2	Sequence 2, Appli	193	196.5	10.0	446	7	US-11-166-412-67	Sequence 67, Appl
121	241.5	12.3	412	7	US-11-170-153-4	Sequence 4, Appli	194	196	9.9	365	6	US-10-875-716-9	Sequence 9, Appli
122	241.5	12.3	412	7	US-11-170-166-4	Sequence 4, Appli	195	195.5	9.9	358	6	US-10-055-877-176	Sequence 176, App
123	241.5	12.3	412	7	US-11-170-351-4	Sequence 4, Appli	196	195.5	9.9	358	7	US-11-174-816-64	Sequence 64, Appl
124	241.5	12.3	415	7	US-11-170-153-2	Sequence 2, Appli	197	195.5	9.9	358	7	US-11-174-819-83	Sequence 83, Appl
125	241.5	12.3	415	7	US-11-170-166-2	Sequence 2, Appli	198	195	9.9	342	7	US-11-174-751-19	Sequence 19, Appl
126	241.5	12.3	415	7	US-11-170-351-2	Sequence 2, Appli	199	194	9.8	358	7	US-11-174-819-17	Sequence 17, Appl
127	241.5	12.3	415	7	US-11-127-877-45	Sequence 45, Appl	200	193.5	9.8	350	7	US-11-165-024-3	Sequence 3, Appli
128	241	12.2	414	6	US-10-515-966-2	Sequence 2, Appli	201	193	9.8	337	6	US-10-875-716-2	Sequence 2, Appli
129	240	12.2	393	7	US-11-073-420-30	Sequence 30, Appl	202	192.5	9.8	333	6	US-10-055-877-178	Sequence 178, App
130	239.5	12.2	342	7	US-11-151-482-3	Sequence 3, Appli	203	192.5	9.8	347	7	US-11-174-816-42	Sequence 42, Appl
131	239	12.1	407	7	US-11-127-877-56	Sequence 56, Appl	204	192.5	9.8	347	7	US-11-174-819-9	Sequence 9, Appli
132	238	12.1	458	6	US-10-877-346-51	Sequence 51, Appl	205	192.5	9.8	351	7	US-11-174-751-6	Sequence 6, Appli
133	236.5	12.0	395	7	US-11-218-281-29	Sequence 29, Appl	206	192.5	9.8	358	7	US-11-174-816-65	Sequence 65, Appl
134	232	11.8	394	7	US-11-183-615-17	Sequence 17, Appl	207	192.5	9.8	358	7	US-11-174-819-84	Sequence 84, Appl
135	231.5	11.8	442	7	US-11-100-640-34	Sequence 34, Appl	208	192.5	9.8	455	6	US-10-987-856-4	Sequence 4, Appli
136	229	11.6	384	7	US-11-073-420-2	Sequence 2, Appli	209	192.5	9.8	455	7	US-11-183-615-7	Sequence 7, Appli
137	228.5	11.6	384	7	US-11-073-420-4	Sequence 4, Appli	210	192.5	9.8	486	6	US-10-877-346-50	Sequence 50, Appl
138	227	11.5	384	7	US-11-073-420-7	Sequence 7, Appli	211	192	9.7	352	6	US-10-627-633-6	Sequence 6, Appli
139	225	11.4	375	6	US-10-987-856-17	Sequence 17, Appl	212	191.5	9.7	348	7	US-11-174-816-48	Sequence 48, Appl
140	223	11.3	384	7	US-11-073-420-8	Sequence 8, Appli	213	191.5	9.7	348	7	US-11-174-819-34	Sequence 34, Appl
141	219	11.1	475	6	US-10-877-346-48	Sequence 48, Appl	214	191.5	9.7	358	7	US-11-174-816-52	Sequence 52, Appl
142	218.5	11.1	429	7	US-11-127-877-51	Sequence 51, Appl	215	191.5	9.7	358	7	US-11-174-819-24	Sequence 24, Appl
143	218.5	11.1	466	7	US-11-127-877-50	Sequence 50, Appl	216	191	9.7	344	7	US-11-174-819-77	Sequence 77, Appl
144	218	11.1	344	7	US-11-174-816-60	Sequence 60, Appl	217	191	9.7	415	6	US-10-627-633-2	Sequence 2, Appli
145	218	11.1	344	7	US-11-174-819-79	Sequence 79, Appl	218	190.5	9.7	358	7	US-11-174-816-51	Sequence 51, Appl
146	216	11.1	389	6	US-10-513-118-2	Sequence 2, Appli	219	190.5	9.7	358	7	US-11-174-819-22	Sequence 22, Appl
147	216	11.0	358	6	US-10-980-388-96	Sequence 96, Appl	220	190	9.6	345	7	US-11-174-816-59	Sequence 59, Appl
148	216	11.0	399	6	US-10-980-388-116	Sequence 116, App	221	190	9.6	345	7	US-11-174-819-78	Sequence 78, Appl
149	214	10.9	337	6	US-10-980-388-115	Sequence 115, App	222	189.5	9.6	345	7	US-11-174-816-44	Sequence 44, Appl
150	213.5	10.8	457	6	US-10-877-346-49	Sequence 49, Appl	223	189.5	9.6	345	7	US-11-174-819-13	Sequence 13, Appl
151	211.5	10.7	345	7	US-11-174-816-15	Sequence 15, Appl	224	189.5	9.6	358	7	US-11-174-819-89	Sequence 89, Appl
152	211.5	10.7	345	7	US-11-174-819-70	Sequence 70, Appl	225	189	9.6	337	7	US-11-174-816-13	Sequence 13, Appl
153	211	10.7	344	7	US-11-174-816-61	Sequence 61, Appl	226	189	9.6	337	7	US-11-174-819-69	Sequence 69, Appl
154	211	10.7	344	7	US-11-174-819-80	Sequence 80, Appl	227	188.5	9.6	339	7	US-11-127-877-49	Sequence 49, Appl
155	211	10.7	345	7	US-11-174-819-16	Sequence 16, Appl	228	188.5	9.6	339	7	US-11-174-816-3	Sequence 3, Appli
156	208.5	10.6	339	7	US-11-174-819-81	Sequence 81, Appl	229	188.5	9.6	339	7	US-11-174-819-67	Sequence 67, Appl
157	208.5	10.6	339	7	US-11-174-819-74	Sequence 74, Appl	230	188.5	9.6	339	7	US-11-174-751-46	Sequence 46, Appl
158	206.5	10.5	342	6	US-10-980-388-118	Sequence 118, App	231	188	9.5	337	7	US-11-174-751-14	Sequence 14, Appl
159	206.5	10.5	342	7	US-11-174-816-18	Sequence 18, Appl	232	188	9.5	358	7	US-11-174-816-66	Sequence 66, Appl
160	206.5	10.5	342	7	US-11-174-816-71	Sequence 71, Appl	233	187.5	9.5	339	6	US-10-055-877-28	Sequence 28, Appl
161	206	10.5	342	7	US-11-174-816-62	Sequence 62, Appl	234	187.5	9.5	348	7	US-10-055-877-174	Sequence 174, App
162	206	10.5	344	7	US-11-174-819-81	Sequence 81, Appl	235	187.5	9.5	348	7	US-11-127-877-48	Sequence 48, Appl
163	205.5	10.4	371	6	US-10-501-035-242	Sequence 242, App	236	187.5	9.5	348	7	US-11-174-819-20	Sequence 20, Appl
164	205.5	10.4	471	6	US-10-995-561-901	Sequence 901, App	237	187.5	9.5	348	7	US-11-174-819-72	Sequence 72, Appl
165	204.5	10.4	339	7	US-11-174-816-40	Sequence 40, Appl	238	187.5	9.5	362	7	US-11-174-816-70	Sequence 70, Appl
166	204.5	10.4	339	7	US-11-174-819-5	Sequence 5, Appli	239	187	9.5	348	7	US-11-174-816-11	Sequence 11, Appl
167	204.5	10.4	344	7	US-11-174-816-47	Sequence 47, Appl	240	187	9.5	358	7	US-11-174-819-85	Sequence 85, Appl
168	204.5	10.4	344	7	US-11-174-819-32	Sequence 32, Appl	241	187	9.5	590	7	US-11-124-368A-183	Sequence 183, App
169	204.5	10.4	358	7	US-11-174-816-68	Sequence 68, Appl	242	187	9.5	590	7	US-11-127-877-54	Sequence 54, Appl
170	204.5	10.4	358	7	US-11-174-819-87	Sequence 87, Appl	243	186.5	9.5	453	7	US-11-055-759-209	Sequence 209, App
171	203	10.3	344	7	US-11-174-816-46	Sequence 46, Appl	244	185.5	9.4	338	6	US-10-055-877-175	Sequence 175, App

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OM protein - protein search, using sw model

Run on: March 29, 2006, 13:57:19 ; Search time 167 Seconds
(without alignments)
935.738 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 1867555

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 1045 summaries

Database : Published Applications AA.Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1823	92.5	344	4	US-10-232-886-9
4	1823	92.5	344	4	US-10-067-800-9
5	1823	92.5	344	4	US-10-135-839-9
6	1823	92.5	344	5	US-10-994-679-9
7	1727.5	87.7	329	3	US-09-725-285-9
8	1727.5	87.7	329	3	US-09-195-662A-9
9	1727.5	87.7	329	3	US-09-339-912A-9
10	1727.5	87.7	329	3	US-09-502-783A-9
11	1727.5	87.7	329	4	US-10-791-905-9
12	1727.5	87.7	329	5	US-10-127-764-9
13	1651.5	83.8	360	3	US-09-131-827A-2
14	1651.5	83.8	360	4	US-10-225-567A-460
15	1651.5	83.8	360	4	US-10-164-649-50
16	1651.5	83.8	360	4	US-10-239-423-64
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21	1651.5	83.8	360	5	US-10-791-166-4
22	1651.5	83.8	360	5	US-10-700-313-8
23	1651.5	83.8	360	5	US-10-486-471-4
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26	1651.5	83.8	359	5	US-10-988-267-24
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29	1645.5	83.5	360	3	US-09-939-226-7	Sequence 7, Appli
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32	1645.5	83.5	360	4	US-10-661-798-7	Sequence 7, Appli
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57	1224	62.1	352	4	US-10-106-623-20	Sequence 20, Appl
58	1224	62.1	352	4	US-10-232-686-2	Sequence 2, Appli
59	1224	62.1	352	4	US-10-086-814-1	Sequence 1, Appli
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83	1224	62.1	352	5	US-10-287-436A-432	Sequence 432, App
84	1224	62.1	352	5	US-10-287-436A-1133	Sequence 1133, Ap
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102	967.5	49.1	355	4	US-10-225-567A-62	Sequence 62, Appl	175	831.5	42.2	360	5	US-10-933-356-20	Sequence 20, Appl
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109	967.5	49.1	355	4	US-10-755-889-582	Sequence 582, App	182	828.5	42.1	360	5	US-10-486-471-8	Sequence 8, Appl
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122	967.5	49.1	355	6	US-11-021-951-160	Sequence 160, App	195	723	36.7	355	5	US-10-893-996-2	Sequence 2, Appl
123	967.5	49.1	375	4	US-10-219-834-78	Sequence 78, Appl	196	723	36.7	355	5	US-10-486-471-16	Sequence 16, Appl
124	940.5	47.7	355	3	US-09-938-719-9	Sequence 9, Appl	197	718	36.4	355	3	US-09-826-503-479	Sequence 479, App
125	940.5	47.7	355	3	US-09-939-226-9	Sequence 9, Appl	198	718	36.4	355	3	US-10-925-095-479	Sequence 479, App
126	940.5	47.7	355	3	US-09-938-703-9	Sequence 9, Appl	199	698	35.4	355	3	US-09-789-482-4	Sequence 4, Appl
127	940.5	47.7	355	4	US-10-661-798-9	Sequence 9, Appl	200	698	35.4	355	3	US-09-789-486-4	Sequence 4, Appl
128	940.5	47.7	355	4	US-10-612-791-9	Sequence 9, Appl	201	698	35.4	355	4	US-10-290-058A-3	Sequence 3, Appl
129	914	46.4	279	4	US-10-174-364-58	Sequence 58, Appl	202	698	35.4	355	4	US-10-251-385-130	Sequence 130, App
130	914	46.4	279	4	US-10-246-583-58	Sequence 58, Appl	203	698	35.4	355	4	US-10-225-567A-249	Sequence 82, Appl
131	911.5	46.3	355	4	US-10-164-649-53	Sequence 53, Appl	204	698	35.4	355	4	US-10-239-423-82	Sequence 367, App
132	899.5	45.7	355	3	US-09-886-319A-13	Sequence 13, Appl	205	698	35.4	355	5	US-10-741-601-367	Sequence 958, App
133	899.5	45.7	355	4	US-10-376-564-13	Sequence 13, Appl	206	698	35.4	355	5	US-10-723-860-958	Sequence 1084, Ap
134	898.5	45.6	379	3	US-09-893-512-12	Sequence 12, Appl	207	698	35.4	355	5	US-10-741-600-1084	Sequence 18, Appl
135	898.5	45.6	379	5	US-10-799-736-12	Sequence 12, Appl	208	698	35.4	355	5	US-10-486-471-18	Sequence 368, App
136	897.5	45.6	355	3	US-10-283-028-2	Sequence 2, Appl	209	698	35.4	362	4	US-10-741-601-368	Sequence 1085, Ap
137	890.5	45.2	355	3	US-09-931-381A-16	Sequence 16, Appl	210	698	35.4	362	5	US-10-741-600-1085	Sequence 4, Appl
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141	886.5	45.0	355	4	US-10-106-623-4	Sequence 4, Appl	214	694	35.2	184	4	US-10-661-798-4	Sequence 4, Appl
142	886.5	45.0	355	4	US-10-039-659-15	Sequence 15, Appl	215	694	35.2	184	4	US-10-612-791-4	Sequence 4, Appl
143	886.5	45.0	355	4	US-10-225-567A-64	Sequence 64, Appl	216	694	35.2	215	3	US-09-938-719-6	Sequence 6, Appl
144	886.5	45.0	355	4	US-10-283-028-4	Sequence 4, Appl	217	694	35.2	215	3	US-09-939-226-6	Sequence 6, Appl
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147	886.5	45.0	355	4	US-10-754-071-15	Sequence 15, Appl	220	694	35.2	215	4	US-10-661-798-18	Sequence 18, Appl
148	886.5	45.0	355	5	US-10-772-037-4	Sequence 4, Appl	221	694	35.2	215	4	US-10-612-791-18	Sequence 6, Appl
149	886.5	45.0	355	5	US-10-767-521-1	Sequence 1, Appl	222	694	35.2	215	4	US-10-612-791-18	Sequence 18, Appl
150	886.5	45.0	355	5	US-10-759-860-15	Sequence 15, Appl	223	693	35.2	355	4	US-10-251-385-232	Sequence 232, App
151	886.5	45.0	355	5	US-10-486-471-6	Sequence 6, Appl	224	645.5	32.8	344	3	US-09-912-025-2	Sequence 2, Appl
152	886.5	45.0	355	5	US-10-988-267-6	Sequence 6, Appl	225	645.5	32.8	344	5	US-10-741-600-840	Sequence 840, App
153	886.5	45.0	356	5	US-10-988-267-22	Sequence 22, App	226	645.5	32.8	344	5	US-10-741-600-841	Sequence 841, App
154	881.5	44.7	355	3	US-09-826-509-475	Sequence 475, App	227	644.5	32.7	344	4	US-10-223-085-16	Sequence 16, Appl
155	881.5	44.7	355	5	US-10-925-095-475	Sequence 475, App	228	644.5	32.7	344	4	US-10-223-084-16	Sequence 16, Appl
156	875	44.4	356	4	US-10-293-050-7	Sequence 7, Appl	229	644.5	32.7	344	4	US-10-223-088-16	Sequence 16, Appl
157	875	44.4	356	5	US-10-491-997-102	Sequence 102, App	230	644.5	32.7	344	4	US-10-223-090-16	Sequence 16, Appl
158	867	44.0	355	4	US-10-450-590-3	Sequence 3, Appl	231	644.5	32.7	344	4	US-10-223-087-16	Sequence 16, Appl
159	862.5	43.8	355	4	US-10-283-028-6	Sequence 6, Appl	232	644.5	32.7	344	4	US-10-225-567A-354	Sequence 354, App
160	858.5	43.6	355	3	US-09-938-719-8	Sequence 8, Appl	233	644.5	32.7	344	4	US-10-223-083-16	Sequence 16, Appl
161	858.5	43.6	355	3	US-09-939-226-8	Sequence 8, Appl	234	644.5	32.7	344	4	US-10-223-089-16	Sequence 16, Appl
162	858.5	43.6	355	3	US-09-938-703-8	Sequence 8, Appl	235	644.5	32.7	344	4	US-10-223-081-16	Sequence 16, Appl
163	858.5	43.6	355	4	US-10-661-798-8	Sequence 8, Appl	236	644.5	32.7	344	4	US-10-223-082-16	Sequence 16, Appl
164	858.5	43.6	355	4	US-10-612-791-8	Sequence 8, Appl	237	644.5	32.7	344	4	US-10-305-654-16	Sequence 16, Appl
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166	831.5	42.2	360	3	US-09-796-744-17	Sequence 17, Appl	239	644.5	32.7	348	4	US-10-039-659-12	Sequence 12, Appl
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171	831.5	42.2	360	4	US-10-164-649-55	Sequence 55, Appl	244	644.5	32.7	417	5	US-10-349-528-16	Sequence 16, Appl
172	831.5	42.2	360	4	US-10-231-452-48	Sequence 48, Appl	245	636.5	32.3	344	4	US-10-095-876A-4	Sequence 396, App
173	831.5	42.2	360	4	US-10-239-423-66	Sequence 66, Appl	246	588	29.8	384	4	US-10-225-567A-396	Sequence 396, App

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OM protein - protein search, using sw model

Run on: March 29, 2006, 13:45:59 ; Search time 48 Seconds
(without alignments)
644.181 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572054

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
(Maximum Match 99.9999%)
Listing first 1045 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1823	92.5	344	2	US-08-466-343D-9
2	1823	92.5	344	2	US-09-502-784A-9
3	1727.5	87.7	329	2	US-09-502-783A-9
4	1727.5	87.7	329	2	US-09-339-912A-9
5	1727.5	87.7	329	2	US-09-195-662A-9
6	1651.5	83.8	360	1	US-08-450-393A-4
7	1651.5	83.8	360	2	US-08-446-669-4
8	1651.5	83.8	360	2	US-09-045-583-50
9	1651.5	83.8	360	2	US-09-534-185-50
10	1651.5	83.8	360	2	US-09-131-827A-2
11	1651.5	83.8	360	2	US-09-625-573-4
12	1651.5	83.8	360	4	PCT-US95-00476-4
13	1651.5	83.8	377	2	US-09-949-016-11221
14	1650.5	83.8	360	2	US-09-131-827A-20
15	1645.5	83.5	360	2	US-08-833-752-7
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17	1645.5	83.5	360	2	US-09-939-226B-7
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21	1614.5	82.0	360	2	US-09-534-185-51
22	1589.5	80.7	347	1	US-08-461-244-3
23	1236	62.7	352	2	US-09-517-605-5
24	1234	62.6	354	2	US-08-724-984A-2
25	1230	62.4	352	2	US-09-045-583-52
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105	698	35.4	355	2	US-09-170-496D-130	Sequence 130, App	178	541.5	27.5	360	1	US-08-202-056-7	Sequence 7, Appl
106	698	35.4	355	2	US-09-917-254-68	Sequence 68, Appl	179	541.5	27.5	360	2	US-09-409-778-4	Sequence 4, Appl
107	698	35.4	355	4	PCT-US93-11153-28	Sequence 28, Appl	180	536.5	27.2	365	2	US-053-219B-8	Sequence 8, Appl
108	698	35.4	355	4	PCT-US93-11153-32	Sequence 32, Appl	181	536.5	27.2	365	2	US-10-039-659A-10	Sequence 10, Appl
109	694	35.2	184	2	US-08-833-752-4	Sequence 4, Appl	182	534.5	27.1	368	2	US-08-709-838-2	Sequence 2, Appl
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116	694	35.2	215	2	US-09-339-226B-6	Sequence 6, Appl	189	530.5	26.9	362	2	US-09-178-637-2	Sequence 2, Appl
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133	584	29.6	378	2	US-09-170-496D-74	Sequence 74, Appl	206	527.5	26.8	337	2	US-09-299-843A-46	Sequence 46, Appl
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135	584	29.6	410	1	US-08-153-848-7	Sequence 7, Appl	208	527.5	26.8	337	4	PCT-US93-11153-46	Sequence 46, App
136	584	29.6	410	2	US-09-399-843A-7	Sequence 7, Appl	209	525	26.6	350	2	US-09-826-509-485	Sequence 485, App
137	584	29.6	410	2	US-09-088-337B-7	Sequence 7, Appl	210	524.5	26.6	350	2	US-09-949-002-305	Sequence 305, App
138	584	29.6	410	4	PCT-US93-11153-7	Sequence 7, Appl	211	524.5	26.6	377	2	US-09-949-002-549	Sequence 549, App
139	580	29.4	378	2	US-09-045-583-5	Sequence 5, Appl	212	523.5	26.6	350	1	US-08-202-056-1	Sequence 1, Appl
140	580	29.4	378	2	US-09-534-185-5	Sequence 5, Appl	213	523.5	26.6	350	1	US-08-076-093A-2	Sequence 2, Appl
141	579	29.4	378	2	US-09-170-496D-204	Sequence 204, App	214	523.5	26.6	350	1	US-08-450-393A-7	Sequence 7, Appl
142	575.5	29.2	378	2	US-09-399-843A-66	Sequence 66, Appl	215	523.5	26.6	350	1	US-08-410-453A-1	Sequence 1, Appl
143	575.5	29.2	378	2	US-09-088-337B-66	Sequence 66, Appl	216	523.5	26.6	350	1	US-08-701-265-2	Sequence 2, Appl
144	573	29.1	359	1	US-08-153-848-24	Sequence 24, Appl	217	523.5	26.6	350	1	US-08-410-454A-1	Sequence 1, Appl
145	573	29.1	359	2	US-09-399-843A-24	Sequence 24, Appl	218	523.5	26.6	350	1	US-08-284-586-2	Sequence 2, Appl
146	573	29.1	359	2	US-09-088-337B-24	Sequence 24, Appl	219	523.5	26.6	350	1	US-08-410-458A-1	Sequence 1, Appl
147	573	29.1	359	4	PCT-US93-11153-24	Sequence 24, Appl	220	523.5	26.6	350	1	US-08-805-478-2	Sequence 2, Appl
148	570	28.9	378	1	US-08-383-751A-2	Sequence 2, Appl	221	523.5	26.6	350	1	US-08-801-238-2	Sequence 2, Appl
149	570	28.9	378	1	US-08-352-678-2	Sequence 2, Appl	222	523.5	26.6	350	1	US-08-801-228-2	Sequence 2, Appl
150	570	28.9	378	2	US-09-045-583-49	Sequence 49, Appl	223	523.5	26.6	350	1	US-08-801-228-2	Sequence 2, Appl
151	570	28.9	378	2	US-09-534-185-49	Sequence 49, Appl	224	523.5	26.6	350	2	US-09-104-296-2	Sequence 2, Appl
152	570	28.9	378	2	US-09-336-954-2	Sequence 2, Appl	225	523.5	26.6	350	2	US-08-446-669-7	Sequence 7, Appl
153	570	28.9	378	2	US-09-329-583B-2	Sequence 2, Appl	226	523.5	26.6	350	4	PCT-US95-00476-7	Sequence 7, Appl
154	570	28.9	378	2	US-09-721-341-7	Sequence 7, Appl	227	523.5	26.5	350	4	US-08-742-011-2	Sequence 2, Appl
155	570	28.9	378	2	US-09-721-341-7	Sequence 7, Appl	228	521.5	26.5	342	1	US-09-275-384B-5	Sequence 5, Appl
156	570	28.9	378	2	PCT-US93-09636-2	Sequence 2, Appl	229	521.5	26.5	342	2	US-09-116-498-2	Sequence 2, Appl
157	570	28.9	378	4	US-09-266-464-2	Sequence 2, Appl	230	521.5	26.5	342	2	US-09-449-437A-2	Sequence 2, Appl
158	569	28.9	357	2	US-09-170-496D-24	Sequence 24, Appl	231	521.5	26.5	342	2	US-09-517-605-9	Sequence 9, Appl
159	569	28.9	357	2	US-09-952-385-2	Sequence 2, Appl	232	521.5	26.5	342	2	US-09-852-156-6	Sequence 6, Appl
160	569	28.9	357	2	US-09-966-755-2	Sequence 2, Appl	233	521.5	26.5	342	2	US-09-852-156-6	Sequence 6, Appl
161	569	28.9	357	2	US-09-522-752-2	Sequence 2, Appl	234	521.5	26.5	342	2	US-09-721-341-9	Sequence 9, Appl
162	569	28.9	357	2	US-09-721-341-6	Sequence 6, Appl	235	521.5	26.5	342	2	US-09-721-495B-9	Sequence 9, Appl
163	569	28.9	359	2	US-09-721-495B-6	Sequence 6, Appl	236	519	26.3	333	2	US-09-170-496D-8	Sequence 8, Appl
164	569	28.9	359	2	US-09-949-016-11223	Sequence 11223, A	237	516.5	26.2	342	2	US-09-116-498-6	Sequence 6, Appl
165	569	28.9	371	2	US-09-170-496D-176	Sequence 176, App	238	516.5	26.2	342	2	US-09-852-156-6	Sequence 6, Appl
166	566	28.7	357	2	US-09-826-509-481	Sequence 481, App	239	516	26.2	342	2	US-09-852-156-6	Sequence 6, Appl
167	566	28.7	369	2	US-09-045-583-48	Sequence 48, Appl	240	513	26.0	342	2	US-09-852-156-4	Sequence 4, Appl
168	554.5	28.1	374	2	US-09-534-185-48	Sequence 48, Appl	241	513	26.0	333	2	US-09-826-509-509	Sequence 509, App
169	554.5	28.1	374	2	US-09-721-341-8	Sequence 8, Appl	242	513	26.0	333	1	US-08-118-270-38	Sequence 38, Appl
170	552.5	28.0	374	2	US-09-721-495B-8	Sequence 8, Appl	243	506	25.7	312	4	PCT-US93-08528-38	Sequence 38, Appl
171	552.5	28.0	374	2	US-07-759-568-1	Sequence 1, Appl	244	506	25.7	312	4	US-08-966-316-18	Sequence 18, Appl
172	541.5	27.5	355	1	US-08-450-393A-8	Sequence 8, Appl	245	484	24.6	350	2	US-09-910-695-8	Sequence 8, Appl
173	541.5	27.5	355	1			246	484	24.6	350	2		

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OM protein - protein search, using sw model

Run on: March 29, 2006, 13:38:29 ; Search time 233 Seconds
(without alignments)
1132.479 Million cell updates/sec

Title: US-10-791-592-2
Perfect score: 1970
Sequence: 1 MLSTSRRPRTNNESEEV.....GKGSIGRAPEASLDKQEGA 374

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 99.9999%
Listing first 1045 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1651.5	83.8	360	2 Q4VB12 HUMAN	Q4VB12 homo sapien
2	1614.5	82.0	360	1 CCR2 MACMU	Q18793 macaca mula
3	1346.5	68.4	373	1 CCR2 RAT	O55193 rattus norv
4	1332.5	67.6	373	1 CCR2 MOUSE	P51683 mus musculus
5	1332.5	67.6	373	2 O54388 MOUSE	Q54388 mus musculus
6	1327.5	67.4	373	2 O6YT42 PIG	O6YT42 sus scrofa
7	1252	63.6	352	2 Q95NC2 CALMO	Q95nc2 callicebus
8	1247	63.3	354	2 Q68G28 RAT	Q68g28 rattus norv
9	1244	63.1	339	2 Q9TQ73 CALJA	Q9tqt3 callithrix
10	1244	63.1	339	2 Q9TUV8 PRIM	Q9tuv8 saguinus sp
11	1244	63.1	352	2 Q6WN98 CALHU	Q6wn98 callithrix
12	1244	63.1	352	2 Q9M2A0 CALJA	Q9mza0 callithrix
13	1244	63.1	354	1 CCR5 MOUSE	P51682 mus musculus
14	1243	63.1	339	2 Q9TUV5 PRIM	Q9tqv5 saguinus sp
15	1243	63.1	352	2 Q95NC4 ATEGE	Q95nc4 ateles geof
16	1241	63.0	352	2 Q6WN93 LEOCH	Q6wn93 leontopithe
17	1241	63.0	352	2 Q6WN96 LEOCH	Q6wn96 leontopithe
18	1241	63.0	352	2 Q6WN97 CEBPY	Q6wn97 cebuella py
19	1240	62.9	339	2 Q9TUV0 PRIM	Q9tuw0 saguinus sp
20	1239	62.9	352	2 Q6YT41 PIG	Q6yt41 sus scrofa
21	1239	62.9	352	2 Q9MZ99 ATESP	Q9mz99 ateles sp
22	1238.5	62.9	339	2 Q9TUV6 PRIM	Q9tuv6 saguinus sp
23	1238	62.8	339	2 Q9TUV1 PRIM	Q9tuw1 saguinus sp
24	1237	62.8	339	2 Q9TUV9 PRIM	Q9tuv9 saguinus sp
25	1236	62.7	339	2 Q9TQW0 HILCO	Q9tqw0 hylobates c
26	1236	62.7	352	1 CCR5 CERTO	O62743 cercocebus
27	1236	62.7	352	1 CCR5 HYLLE	Q97883 hylobates l
28	1236	62.7	352	2 Q6WN92 LEOCH	Q6wn92 leontopithe
29	1236	62.7	352	2 Q6WN94 LEOCY	Q6wn94 leontopithe
30	1236	62.7	352	2 Q71RS2 PRIM	Q71rs2 cercocebus
31	1236	62.7	352	2 Q6H2T9 SAISC	Q6hzt9 saimiri sci

32	1235	62.7	339	2	Q9TSN3 MACPA	O9ten3 macaca fasc
33	1235	62.7	339	2	Q77776 PRIM	O77776 cercocebus
34	1234	62.6	339	2	Q9TUV5 PRIM	O9tuv5 saguinus sp
35	1234	62.6	339	2	Q6WN95 LEOCH	O6wn95 leontopithe
36	1233	62.6	339	2	Q9TUV2 ALOCA	O9tuv2 alouatta ca
37	1233	62.6	339	2	Q95NE1 CERTO	O95ne1 cercocebus
38	1232	62.5	339	2	Q9TUV9 MACMU	O9tuv9 macaca mula
39	1232	62.5	339	2	Q9TUV0 AOTTR	O9tuv0 aotus trivi
40	1232	62.5	339	2	Q9TUV4 CALJA	O9tuv4 callithrix
41	1232	62.5	339	2	Q9TUX0 HILCO	O9tux0 hylobates c
42	1232	62.5	339	2	Q6WN91 BRAAR	O6wn91 brachyteles
43	1231	62.5	339	2	Q9TUV9 HILCO	O9tuv9 hylobates c
44	1231	62.5	339	2	CCR5 HYLML	O95nc0 hylobates m
45	1231	62.5	339	2	Q95NC9 ALOSE	O95nc9 alouatta se
46	1231	62.5	339	2	Q9XT12 CERNE	Q9xt12 cercoptithec
47	1230	62.4	339	2	Q9TQ70 MACFA	O9tqt0 macaca fasc
48	1230	62.4	339	2	Q9TQ71 MACMU	O9tqt1 macaca mula
49	1230	62.4	339	2	Q9TQ72 MACNE	O9tqt2 macaca neme
50	1230	62.4	339	2	Q9TQ72 PONPY	O9tqt2 pongo pygma
51	1230	62.4	339	2	Q9TQ74 PANTR	O9tqt4 pan troglod
52	1230	62.4	339	2	Q9TUV1 MACMU	O9tuw1 macaca mula
53	1230	62.4	339	2	Q9TUV4 MACMU	O9tuw4 macaca mula
54	1230	62.4	339	2	Q9TUV5 PRIM	O9tuv5 macaca fusc
55	1230	62.4	339	2	Q9TUV7 PRIM	O9tuv7 macaca fusc
56	1230	62.4	339	2	Q9TUV7 PANTR	O9tuv7 pan troglod
57	1230	62.4	339	2	CCR5 HYLSE	O95nc5 hylobates s
58	1230	62.4	339	2	CCR5 MACFA	P61814 macaca fasc
59	1230	62.4	339	2	CCR5 MACMU	P61813 macaca mula
60	1230	62.4	339	2	CCR5 MACNE	P61815 macaca neme
61	1230	62.4	339	2	CCR5 PANPA	P60574 pan paniscu
62	1230	62.4	339	2	CCR5 PANTR	P60574 pan troglod
63	1230	62.4	339	2	CCR5 PONPA	P61756 pongo pygma
64	1230	62.4	339	2	CCR5 PONPY	O97881 pongo pygma
65	1230	62.4	339	2	Q97975 MACAR	O97975 macaca arc
66	1230	62.4	339	2	Q53280 MACNE	O53280 macaca neme
67	1230	62.4	339	2	Q54809 MACFA	O54809 macaca fasc
68	1230	62.4	339	2	Q5MD63 BOVIN	O5md63 bos taurus
69	1230	62.4	339	2	Q71T22 PONPP	Q71t22 pongo pygma
70	1230	62.4	339	2	Q71T27 MACNG	Q71t27 macaca nigr
71	1230	62.4	339	2	Q71T28 MACTO	Q71t28 macaca tonk
72	1230	62.4	339	2	Q71T29 MACSI	Q71t29 macaca sini
73	1230	62.4	339	2	Q71J33 MACAS	Q71j33 macaca assa
74	1230	62.4	339	2	CCR5 RAT	O08556 rattus norv
75	1229	62.4	339	2	Q9TUV2 PRIM	O9tuv2 saguinus sp
76	1228	62.3	339	2	Q9TQ72 GORGO	O9tqt2 gorilla gor
77	1228	62.3	339	2	Q9TQ72 PAPP	O9tqt2 papio papio
78	1228	62.3	339	2	Q9TQV3 CERMO	O9tqv3 cercoptithec
79	1228	62.3	339	2	Q9TQV6 COLGU	O9tqv6 colobus gue
80	1228	62.3	339	2	Q9TUV6 PANTR	O9tuv6 pan troglod
81	1228	62.3	339	2	CCR5 GORGO	P56439 gorilla gor
82	1228	62.3	339	2	CCR5 LOPAT	P61755 lophocebus
83	1228	62.3	339	2	CCR5 PAPAN	P68269 papio amabi
84	1228	62.3	339	2	CCR5 PAPA	P68270 papio hamad
85	1228	62.3	339	2	Q18770 PANTR	O18770 pan troglod
86	1228	62.3	339	2	Q549B2 GORGO	O549b2 gorilla gor
87	1228	62.3	339	2	Q71T20 GORBE	Q71t20 gorilla gor
88	1228	62.3	339	2	Q71T21 PRIM	Q71t21 gorilla gor
89	1228	62.3	339	2	Q71UI8 PRIM	Q71ui8 cercoptithec
90	1228	62.3	339	2	Q95NC8 COLPO	O95nc8 colobus pol
91	1228	62.3	339	2	Q9TV49 CERGA	O9tv49 cercocebus
92	1227	62.3	339	2	Q9TQX2 ERYPA	O9tqx2 erythrocebu
93	1227	62.3	339	2	Q9TQX3 MANSP	O9tqx3 mandrillus
94	1227	62.3	339	2	Q9TUV3 CALJA	O9tuv3 callithrix
95	1227	62.3	339	2	Q95ND0 ERYPA	O95nd0 erythrocebu
96	1227	62.3	339	2	Q95ND2 MANLE	O95nd2 mandrillus
97	1227	62.3	339	2	Q9TQ77 ERYPA	O9tq77 erythrocebu
98	1226	62.2	339	2	Q9UN26 HUMAN	O9un26 homo sapien
99	1226	62.2	339	2	Q95ND1 MANSP	O95nd1 mandrillus
100	1226	62.2	339	2	Q9BGN6 PRIM	O9bgn6 cercoptithec
101	1226	62.2	339	2	Q9TV93 MACAR	O9tv93 macaca arc
102	1226	62.2	339	2	Q9TUV5 PAPP	O9tuv5 papio papio
103	1226	62.2	339	2	Q9TUV3 MACNE	O9tuv3 macaca neme
104	1225	62.2	339	2	Q9TUV3 MACNE	O9tuv3 macaca neme

105	1225	62.2	352	2	Q9XS99_9PRIM	Q9XS99 gorilla gor	178	1217	61.8	339	2	Q9TUR0_CERMO	Q9tur0 cercopithec
106	1224	62.1	339	2	Q9UBT9_HUMAN	Q9ubt9 homo sapien	179	1217	61.8	339	2	Q9TUR4_MANS	Q9tur4 mandrillus
107	1224	62.1	339	2	Q9UN23_HUMAN	Q9un23 homo sapien	180	1217	61.8	339	2	Q9TUU9_CERDI	Q9tuu9 cercopithec
108	1224	62.1	339	2	Q9UN28_HUMAN	Q9un28 homo sapien	181	1217	61.8	352	2	Q9TV46_CERNE	Q9tv46 cercopithec
109	1224	62.1	339	2	Q9TQV0_PAPPA	Q9tqv0 papio papio	182	1216	61.7	339	2	Q9TQU7_9PRIM	Q9tqu7 cercopithec
110	1224	62.1	339	2	Q9TUR1_CERMO	Q9tur1 cercopithec	183	1216	61.7	339	2	Q9TSQ1_CERAE	Q9tsq1 cercopithec
111	1224	62.1	339	2	Q9TUR9_9PRIM	Q9tur9 saguinus sp	184	1216	61.7	339	2	Q9TUT2_MACNE	Q9tut2 macaca neme
112	1224	62.1	339	2	Q9TUS9_PAPPA	Q9tus9 papio papio	185	1216	61.7	352	2	Q5EKM8_HUMAN	Q5ekm8 homo sapien
113	1224	62.1	339	2	Q9TUT1_MACNE	Q9tut1 macaca neme	186	1215	61.7	339	2	Q9TUQ5_ERYPA	Q9tuq5 erythrocebu
114	1224	62.1	339	2	Q9TUV1_AOTTR	Q9tuv1 aotus trivi	187	1215	61.7	352	2	Q9BGN5_CERMI	Q9bgn5 cercopithec
115	1224	62.1	339	2	Q9TUM5_PANTR	Q9tums pan troglod	188	1215	61.7	352	2	Q9TV43_9PRIM	Q9tv43 cercopithec
116	1224	62.1	352	1	CCRS_HUMAN	F51681 homo sapien	189	1214	61.6	352	2	Q9TQX0_CERAE	Q9tqx0 cercopithec
117	1224	62.1	352	1	CCRS_PYGNE	Q97882 pygathrix n	190	1213	61.6	352	2	Q5QIP0_HUMAN	Q5qip0 homo sapien
118	1224	62.1	352	2	Q5EKM9_HUMAN	Q5ekm9 homo sapien	191	1212	61.5	339	2	Q9TSQ3_CERAE	Q9tsq3 cercopithec
119	1224	62.1	352	2	Q5QIP1_HUMAN	Q5qip1 homo sapien	192	1212	61.5	339	2	Q9TUS6_PAPPA	Q9tus6 papio papio
120	1224	62.1	352	2	Q9SNC1_THEGE	Q9snc1 theropithec	193	1212	61.5	352	2	Q9TV47_9PRIM	Q9tv47 cercopithec
121	1224	62.1	352	2	Q9SNC3_MIOTA	Q9snc3 miopithecus	194	1211	61.5	339	2	Q9UN25_HUMAN	Q9un25 homo sapien
122	1224	62.1	352	2	Q9XT14_COLGU	Q9xt14 colobus gue	195	1211	61.5	339	2	Q9UNT0_MACNE	Q9unt0 macaca neme
123	1223	62.1	339	2	Q9TUR3_ERYPA	Q9tur3 erythrocebu	196	1211	61.5	352	1	CCRS_CERAE	P56493 cercopithec
124	1223	62.1	339	2	Q9TUT4_MACNE	Q9tut4 macaca neme	197	1210	61.4	339	2	Q9TUR6_CERAE	Q9tur6 cercopithec
125	1223	62.1	339	2	Q9TUU0_MACMU	Q9tuu0 macaca mula	198	1210	61.4	339	2	Q9TUR7_CERAE	Q9tur7 cercopithec
126	1223	62.1	339	2	Q9TUU3_MACMU	Q9tuu3 macaca mula	199	1209	61.4	339	2	Q9TUR8_CERAE	Q9tur8 cercopithec
127	1223	62.1	339	2	Q9TUU8_CERDI	Q9tuu8 cercopithec	200	1207.5	61.3	351	2	Q5EKN0_HUMAN	Q5ekn0 homo sapien
128	1223	62.1	339	2	Q9TUM4_PANTR	Q9tum4 pan troglod	201	1206.5	61.2	339	2	Q9TUS3_LEMVA	Q9tus3 lemur catta
129	1223	62.1	339	2	Q9TUX1_HYLCO	Q9tux1 hyllobates c	202	1203	61.1	352	2	Q9WZA2_CERAE	Q9wza2 cercopithec
130	1223	62.1	340	2	Q9TUU2_MACMU	Q9tuu2 macaca mula	203	1202.5	61.0	339	2	Q9TQU3_LEMCA	Q9tqu3 lemur catta
131	1223	62.1	352	1	CCRS_PYGBI	Q97880 pygathrix b	204	1201	61.0	352	2	Q9TSQ7_CERAE	Q9tsq7 cercopithec
132	1223	62.1	352	1	CCRS_SEMEN	F61757 semopithec	205	1196	60.7	352	2	Q9TV45_9PRIM	Q9tv45 cercopithec
133	1223	62.1	352	1	CCRS_TRAFR	Q97878 trachypithe	206	1195.5	60.7	339	2	Q9TUS4_LEMVA	Q9tus4 lemur varie
134	1223	62.1	352	1	CCRS_TYRAPH	Q97879 trachypithe	207	1194.5	60.6	339	2	Q9TUS0_LEMVA	Q9tus0 lemur varie
135	1223	62.1	352	2	Q97962_PYGAV	Q97962 pygathrix a	208	1194.5	60.6	339	2	Q9TUS1_LEMVA	Q9tus1 lemur varie
136	1223	62.1	352	2	Q71T26_TRACV	Q71t26 trachypithe	209	1192	60.5	334	2	Q97724_FELCA	Q97724 felis silve
137	1223	62.1	352	2	Q7J184_CERPR	Q7j184 cercopithec	210	1179.5	59.9	339	2	Q9TUS2_LEMCA	Q9tus2 lemur catta
138	1223	62.1	352	2	Q7JJ34_PYGRO	Q7jj34 pygathrix r	211	1176	59.7	344	2	Q9TJ30_CERTO	Q9tj30 cercocebus
139	1223	62.1	352	2	Q9TV50_PANTR	Q9tv50 pan troglod	212	1176	59.7	344	2	Q9TQR8_9PRIM	Q9tqr8 cercocebus
140	1223	62.1	352	2	Q9XS35_MACNE	Q9xs35 macaca neme	213	1175	59.6	344	2	Q77833_9PRIM	Q77833 cercocebus
141	1223	62.1	352	2	Q9XT76_9PRIM	Q9xt76 cercopithec	214	1172.5	59.5	352	2	Q5ECR9_CANFA	Q5ecr9 canis famil
142	1222	62.0	339	2	Q9TUM8_GORGO	Q9tum8 gorilla gor	215	1165.5	59.2	352	2	Q5KSX8_CANFA	Q5ksx8 canis famil
143	1222	62.0	352	2	Q9MZA1_LAGLA	Q9mza1 lagethrix l	216	1163	59.0	316	2	Q9TUV7_9PRIM	Q9tuv7 saguinus sp
144	1221	62.0	339	2	Q9UBJ7_HUMAN	Q9ubj7 homo sapien	217	1158.5	58.8	352	2	Q867D6_FELCA	Q867d6 felis silve
145	1221	62.0	339	2	Q9UN27_HUMAN	Q9un27 homo sapien	218	1128.5	57.3	351	2	Q97774_FELCA	Q97774 felis silve
146	1221	62.0	339	2	Q9TUS8_PAPPA	Q9tus8 papio papio	219	1103.5	56.0	333	2	O14694_HUMAN	O14694 homo sapien
147	1221	62.0	339	2	Q9TUT5_MACNE	Q9tut5 macaca neme	220	997.5	50.6	354	2	Q702H7_CHICK	Q702h7 gallus gall
148	1221	62.0	339	2	Q9TUT6_9PRIM	Q9tut6 macaca fusc	221	994	50.5	359	1	CCR3_CANFA	Q64h34 canis famil
149	1221	62.0	352	2	Q95NC7_NASLA	Q95nc7 nasalis lar	222	969	49.2	359	1	Q5KSX7_CANFA	Q5ksx7 canis famil
150	1221	62.0	352	2	Q9TV44_ERYPA	Q9tv44 erythrocebu	223	967.5	49.1	355	1	CCR1_HUMAN	P32246 homo sapien
151	1221	62.0	352	2	Q9XT13_PAPAN	Q9xt13 papio anubi	224	967.5	49.1	355	2	Q5U003_HUMAN	Q5u003 homo sapien
152	1220	61.9	339	2	Q9UN24_HUMAN	Q9un24 homo sapien	225	956	48.5	354	2	Q6YST0_PIG	Q6yst0 sus scrofa
153	1220	61.9	339	2	Q9TQU4_CERAE	Q9tqu4 cercopithec	226	955	48.5	351	2	Q9MYJ9_RABIT	Q9myj9 oryctolagus
154	1220	61.9	339	2	Q9TQU5_9PRIM	Q9tqu5 cercopithec	227	955	48.5	355	2	Q9MYJ8_CALJA	Q9myj8 callithrix
155	1220	61.9	339	2	Q9TSN2_MACFA	Q9tsn2 macaca fasc	228	951.5	48.3	359	1	CCR3_MOUSE	P51678 mus musculus
156	1220	61.9	339	2	Q9TQU9_CERMO	Q9tqu9 cercopithec	229	950.5	48.2	359	2	Q8X3M7_MOUSE	Q8x3m7 mus musculus
157	1220	61.9	339	2	Q9TUR2_ERYPA	Q9tur2 erythrocebu	230	945	48.0	359	1	CCR3_RAT	O54814 rattus norv
158	1220	61.9	339	2	Q9TUT6_MACNE	Q9tut6 macaca neme	231	941.5	47.8	359	2	Q8BBH8_MOUSE	Q8bbh8 m mus muscu
159	1220	61.9	339	2	Q9TUT7_MACMU	Q9tut7 macaca mula	232	932.5	47.3	358	2	Q9N0M0_OVIS	Q9n0m0 ovis aries
160	1220	61.9	352	1	CCRS_CERPY	Q9tv42 cercopithec	233	931.5	47.3	358	1	CCR3_CAVPO	Q9z213 cavia porce
161	1220	61.9	352	2	Q95NE8_9PRIM	Q95ne8 cercopithec	234	920.5	46.7	355	2	Q9JLY8_RAT	Q9jly8 rattus norv
162	1220	61.9	352	2	Q9TSK1_CERAE	Q9tsk1 cercopithec	235	919.5	46.7	355	2	Q8BVM4_MOUSE	Q8bvm4 mus musculus
163	1219	61.9	339	2	Q9TQU6_ERYPA	Q9tqu6 erythrocebu	236	915.5	46.5	352	2	Q640C1_XENLA	Q640c1 xenopus lae
164	1219	61.9	339	2	Q9TUS7_ALOCA	Q9tus7 alouatta ca	237	914.5	46.4	358	2	Q75ZH4_PIG	Q75zh4 s mus muscu
165	1219	61.9	339	2	Q9TUS7_PAPPA	Q9tus7 papio papio	238	913.5	46.4	355	2	Q6ZWR7_MOUSE	Q6zwr7 m mus muscu
166	1219	61.9	352	2	Q5QIN9_HUMAN	Q5qin9 homo sapien	239	911.5	46.3	355	1	CCR1_MACMU	P56482 macaca mula
167	1219	61.9	352	2	Q9MZA3_HYLGA	Q9mza3 hyllobates a	240	908.5	46.1	355	2	Q8BMH9_MOUSE	Q8bmh9 mus musculus
168	1219	61.9	352	2	Q9TV48_9PRIM	Q9tv48 cercopithec	241	902.5	45.8	355	2	Q4FK73_MOUSE	Q4fk73 mus musculus
169	1218	61.8	339	2	Q9TQU6_CERAE	Q9tqu6 cercopithec	242	899.5	45.7	355	1	CCR1_MOUSE	P51677 homo sapien
170	1218	61.8	339	2	Q9TSQ2_CERAE	Q9tsq2 cercopithec	243	886.5	45.0	355	1	CCR3_HUMAN	P51677 homo sapien
171	1218	61.8	339	2	Q9TUT8_MACMU	Q9tut8 macaca mula	244	876	44.5	355	1	CCR3_MACMU	P56483 macaca mula
172	1218	61.8	352	2	O18771_PANTR	O18771 pan troglod	245	872.5	44.3	355	2	Q8WMR4_MACFA	Q8wmr4 macaca fasc
173	1218	61.8	352	2	O18772_PANTR	O18772 pan troglod	246	872	44.3	355	2	Q7JH47_MACMU	Q7jh47 macaca mula
174	1218	61.8	352	2	Q9SNC6_TRAJO	Q9snc6 trachypithe	247	872	44.3	355	2	Q8MXK5_MACFA	Q8mxk5 macaca fasc
175	1217	61.8	339	2	Q9TSQ4_CERAE	Q9tsq4 cercopithec	248	871.5	44.2	355	2	Q8WMR5_MACFA	Q8wmr5 macaca fasc
176	1217	61.8	339	2	Q9TQU4_ERYPA	Q9tqu4 erythrocebu	249	871	44.2	355	2	Q8MJU6_MACFA	Q8mju6 macaca fasc
177	1217	61.8	339	2	Q9TQU8_9PRIM	Q9tqu8 cercopithec	250	867	44.0	355	1	CCR3_CERAE	P56492 cercopithec

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 29, 2006, 14:01:34 ; Search time 232 Seconds
(without alignments)
1137.360 Million cell updates/sec

Title: US-10-791-592-2
Perfect score: 374
Sequence: 1 MLSTSRFRINTNESGEV.....GKSGSIGRAPEASLDQKEGA 374

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 10

Total number of hits satisfying chosen parameters: 298

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 90 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
1	374	100.0	374	1	CCR2_HUMAN	P41597 homo sapien
2	313	83.7	360	2	Q4VBL2_HUMAN	Q4VBL2 homo sapien
3	105	28.1	105	2	Q6Y3M6_PANTR	Q6Y3M6 pan troglod
4	105	28.1	105	2	Q6Y3N4_ERYPA	Q6Y3N4 gorilla gor
5	100	26.7	105	2	Q6Y3M7_PANTR	Q6Y3M7 pan troglod
6	93	24.9	140	2	Q95950_HUMAN	Q95950 homo sapien
7	88	23.5	105	2	Q6Y3M9_PONPY	Q6Y3M9 pongo pygma
8	59	15.8	105	2	Q6Y3M3_MACMU	Q6Y3M3 macaca mula
9	59	15.8	105	2	Q6Y3M5_PAPHA	Q6Y3M5 papio hamad
10	59	15.8	105	2	Q6Y3N0_MACFA	Q6Y3N0 macaca fusc
11	59	15.8	360	1	CCR2_MACMU	CCR2 macaca mula
12	51	13.6	86	2	Q6Y3N5_CALJA	Q6Y3N5 callithrix
13	49	13.1	105	2	Q6Y3N1_HYLCO	Q6Y3N1 hylobates
14	47	12.6	373	1	CCR2_RAT	CCR2 rattus norv
15	46	12.3	316	2	Q9TVU7_9PRIM	Q9TVU7 saguinus sp
16	46	12.3	339	2	Q9TVU5_9PRIM	Q9TVU5 saguinus sp
17	46	12.3	339	2	Q9TVU6_9PRIM	Q9TVU6 saguinus sp
18	46	12.3	339	2	Q9TVU8_9PRIM	Q9TVU8 saguinus sp
19	46	12.3	339	2	Q9TVU9_9PRIM	Q9TVU9 saguinus sp
20	46	12.3	339	2	Q9TVU0_9PRIM	Q9TVU0 saguinus sp
21	46	12.3	339	2	Q9TVU1_9PRIM	Q9TVU1 saguinus sp
22	46	12.3	373	2	Q6YT42_PIG	Q6YT42 sus scrofa
23	43	11.5	339	2	Q9TVU2_9PRIM	Q9TVU2 saguinus sp
24	43	11.5	373	1	CCR2_MOUSE	CCR2 mus musculu
25	43	11.5	373	2	Q543S8_MOUSE	Q543S8 mus musculu
26	39	10.4	334	2	Q9TVU7_ERYPA	Q9TVU7 erythrocebu
27	39	10.4	339	2	Q9TVU2_GORGO	Q9TVU2 gorilla gor
28	39	10.4	339	2	Q9TVU0_MACFA	Q9TVU0 macaca fusc
29	39	10.4	339	2	Q9TVU1_MACMU	Q9TVU1 macaca mula
30	39	10.4	339	2	Q9TVU2_MACNE	Q9TVU2 macaca neme
31	39	10.4	339	2	Q9TVU3_CALJA	Q9TVU3 callithrix

32	39	10.4	339	2	Q9TVU4_CERAE	Q9TVU4 cercopithec
33	39	10.4	339	2	Q9TVU5_9PRIM	Q9TVU5 cercopithec
34	39	10.4	339	2	Q9TVU6_CERAE	Q9TVU6 cercopithec
35	39	10.4	339	2	Q9TVU7_9PRIM	Q9TVU7 cercopithec
36	39	10.4	339	2	Q9TVU0_PAPPA	Q9TVU0 papio papio
37	39	10.4	339	2	Q9TVU2_CERMO	Q9TVU2 cercopithec
38	39	10.4	339	2	Q9TVU3_CERMO	Q9TVU3 cercopithec
39	39	10.4	339	2	Q9TVU6_COLGU	Q9TVU6 colobus gue
40	39	10.4	339	2	Q9TVU0_HYLCO	Q9TVU0 hylobates c
41	39	10.4	339	2	Q9TVU2_PONPY	Q9TVU2 pongo pygma
42	39	10.4	339	2	Q9TVU4_PANTR	Q9TVU4 pan troglod
43	39	10.4	339	2	Q9TVU2_ERYPA	Q9TVU2 erythrocebu
44	39	10.4	339	2	Q9TVU3_MANSF	Q9TVU3 mandrillus
45	39	10.4	339	2	Q9TVU3_MACFA	Q9TVU3 macaca fusc
46	39	10.4	339	2	Q9TVU1_CERAE	Q9TVU1 cercopithec
47	39	10.4	339	2	Q9TVU2_CERAE	Q9TVU2 cercopithec
48	39	10.4	339	2	Q9TVU3_CERAE	Q9TVU3 cercopithec
49	39	10.4	339	2	Q9TVU4_CERAE	Q9TVU4 cercopithec
50	39	10.4	339	2	Q9TVU6_ERYPA	Q9TVU6 erythrocebu
51	39	10.4	339	2	Q9TVU8_9PRIM	Q9TVU8 cercopithec
52	39	10.4	339	2	Q9TVU9_CERMO	Q9TVU9 cercopithec
53	39	10.4	339	2	Q9TVU0_CERMO	Q9TVU0 cercopithec
54	39	10.4	339	2	Q9TVU1_CERMO	Q9TVU1 cercopithec
55	39	10.4	339	2	Q9TVU2_ERYPA	Q9TVU2 erythrocebu
56	39	10.4	339	2	Q9TVU3_ERYPA	Q9TVU3 erythrocebu
57	39	10.4	339	2	Q9TVU4_MANSF	Q9TVU4 mandrillus
58	39	10.4	339	2	Q9TVU6_CERAE	Q9TVU6 cercopithec
59	39	10.4	339	2	Q9TVU7_CERAE	Q9TVU7 cercopithec
60	39	10.4	339	2	Q9TVU8_CERAE	Q9TVU8 cercopithec
61	39	10.4	339	2	Q9TVU9_9PRIM	Q9TVU9 saguinus sp
62	39	10.4	339	2	Q9TVU9_PAPPA	Q9TVU9 papio papio
63	39	10.4	339	2	Q9TVU0_MACNE	Q9TVU0 macaca neme
64	39	10.4	339	2	Q9TVU2_MACNE	Q9TVU2 macaca neme
65	39	10.4	339	2	Q9TVU3_MACNE	Q9TVU3 macaca neme
66	39	10.4	339	2	Q9TVU4_MACNE	Q9TVU4 macaca neme
67	39	10.4	339	2	Q9TVU7_MACMU	Q9TVU7 macaca mula
68	39	10.4	339	2	Q9TVU8_MACMU	Q9TVU8 macaca mula
69	39	10.4	339	2	Q9TVU9_MACMU	Q9TVU9 macaca mula
70	39	10.4	339	2	Q9TVU0_MACMU	Q9TVU0 macaca mula
71	39	10.4	339	2	Q9TVU1_MACMU	Q9TVU1 macaca mula
72	39	10.4	339	2	Q9TVU3_MACMU	Q9TVU3 macaca mula
73	39	10.4	339	2	Q9TVU4_MACMU	Q9TVU4 macaca mula
74	39	10.4	339	2	Q9TVU5_9PRIM	Q9TVU5 macaca fusc
75	39	10.4	339	2	Q9TVU6_9PRIM	Q9TVU6 macaca fusc
76	39	10.4	339	2	Q9TVU7_9PRIM	Q9TVU7 macaca fusc
77	39	10.4	339	2	Q9TVU8_CERDI	Q9TVU8 cercopithec
78	39	10.4	339	2	Q9TVU9_CERDI	Q9TVU9 cercopithec
79	39	10.4	339	2	Q9TVU0_AOTTR	Q9TVU0 aotus trivi
80	39	10.4	339	2	Q9TVU1_AOTTR	Q9TVU1 aotus trivi
81	39	10.4	339	2	Q9TVU3_PONPY	Q9TVU3 pongo pygma
82	39	10.4	339	2	Q9TVU4_PANTR	Q9TVU4 pan troglod
83	39	10.4	339	2	Q9TVU6_PANTR	Q9TVU6 pan troglod
84	39	10.4	339	2	Q9TVU7_PANTR	Q9TVU7 pan troglod
85	39	10.4	339	2	Q9TVU8_GORGO	Q9TVU8 gorilla gor
86	39	10.4	339	2	Q9TVU0_HYLCO	Q9TVU0 hylobates c
87	39	10.4	340	2	Q9TVU2_MACMU	Q9TVU2 macaca mula
88	39	10.4	352	1	CCR5_CERAP	P56493 cercopithec
89	39	10.4	352	1	CCR5_CERPY	Q9TV42 cercopithec
90	39	10.4	352	1	CCR5_CERTO	O62743 cercocebus

ALIGNMENTS

RESULT 1
CCR2_HUMAN
ID_CCR2_HUMAN STANDARD; PRT; 374 AA.
AC P41597;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).

GN Name=CCR2; Synonyms=CMKBR2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=94195821; PubMed=8146186;
RX Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,
RA Coughlin S.R.;
RT "Molecular cloning and functional expression of two monocyte
RT chemoattractant protein 1 receptors reveals alternative splicing of
RT the carboxyl-terminal tails.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).
[2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=94324942; PubMed=8048929;
RX Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;
RA "cDNA cloning and functional expression of a human monocyte
RT chemoattractant protein 1 receptor".
RL Biochem. Biophys. Res. Commun. 202:1156-1162(1994).
[3]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RX Wong L.-M., Myers S.J., Teou C.-L., Gosling J., Arai H., Charo I.F.;
RA "Organization and differential expression of the human monocyte
RT chemoattractant protein 1 receptor gene. Evidence for the role of the
RT carboxyl-terminal tail in receptor trafficking".
RL J. Biol. Chem. 272:1038-1045(1997).
[4]
RN NUCLEOTIDE SEQUENCE.
RP McCombie M.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA Sagripanti J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[5]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS ILE-64 AND GLU-355.
RX Riuder M.J., Arnel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Raikumar N., Toth E.J., Yi Q., Nickerson D.A.;
RT "SeattleSNPs NHLBI HUG6682 program for genomic applications, UW-
RT FHRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM A).
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Falmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[7]
RN SULFATION OF TYR-26, AND N-GLYCOSYLATION.
RP MEDLINE=20501139; PubMed=11046064;

RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
RA Chakravarty L., Kolattukudy P.B.;
RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
RT has tyrosine sulfation in a conserved extracellular N-terminal
RT region.";
RL J. Immunol. 165:5295-5303(2000).
CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
CC Transduces a signal by increasing the intracellular calcium ions
CC level. Alternative coreceptor with CD4 for HIV-1 infection.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=P41597-1; Sequence=Displayed;
CC Name=B;
CC IsoId=P41597-2; Sequence=VSP_001893;
CC -!- PTM: N-glycosylated.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; U03882; AAA19119.1; -; mRNA.
CC EMBL; U03905; AAA19120.1; -; mRNA.
CC EMBL; D29984; BAA06253.1; -; mRNA.
CC EMBL; U80924; AAC51637.1; -; Genomic DNA.
CC EMBL; U80924; AAC51636.1; -; Genomic DNA.
CC EMBL; U95626; AAB57791.1; -; Genomic DNA.
CC EMBL; U95626; AAB57792.1; -; Genomic DNA.
CC EMBL; AF545480; AAN16400.1; -; Genomic DNA.
CC EMBL; BC074751; AAH74751.1; -; mRNA.
CC EMBL; U138450; U138450.
CC EMBL; J02443; J02443.
CC PIR; JC2443; JC2443.
CC PDB; 1KAD; Model; A=1-313.
CC PDB; 1KPI; Model; A=1-313.
CC HGNC; HGNC:1603; CCR2.
CC MIM; 601267; -;
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005886; C:plasma membrane; TAS.
CC GO; GO:0005625; C:soluble fraction; TAS.
CC GO; GO:0004950; F:chemokine receptor activity; TAS.
CC GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .; TAS.
CC GO; GO:0006968; P:cellular defense response; TAS.
CC GO; GO:0006955; P:chemotaxis; TAS.
CC GO; GO:0006954; P:inflammatory response; TAS.
CC GO; GO:0007259; P:JAK-STAT cascade; TAS.
CC GO; GO:0007194; P:negative regulation of adenylate cyclase ac. . .; TAS.
CC GO; GO:0007204; P:positive regulation of G-protein coupled receptor;
CC InterPro; IPR002327; CC_2 receptor.
CC InterPro; IPR000355; Chkline receptor.
CC InterPro; IPR00276; GPCR Rhodopsin.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00657; CCHEMOKINER.
CC PRINTS; PR01107; CHEMOKINER2.
CC PRINTS; PR00237; GPCR RHODOPSIN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPTOR F1_2; 1.
CC 3D-structure; Alternative splicing; G-protein coupled receptor;
KW Glycoprotein; Polymorphism; Receptor; Sulfation; Transducer;
KW Transmembrane.
FT TOPO_DOM 1 42 Extracellular (Potential).
FT TRANSMEM 43 80 1 (Potential).
FT TOPO_DOM 71 80 Cytoplasmic (Potential).
FT TRANSMEM 81 100 2 (Potential).
FT TOPO_DOM 101 114 Extracellular (Potential).
FT TRANSMEM 115 136 3 (Potential).
FT TOPO_DOM 137 153 Cytoplasmic (Potential).
FT TRANSMEM 154 178 4 (Potential).
FT TOPO_DOM 179 206 Extracellular (Potential).
FT TRANSMEM 207 226 5 (Potential).

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: March 29, 2006, 14:04:54 ; Search time 41 Seconds
(without alignments)
877.685 Million cell updates/sec
Title: US-10-791-592-2
Perfect score: 374
Sequence: 1 MLSTSRFPRTNTEGEEV.....GKGSIGRAPEASLDQKEGA 374

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0
Searched: 283416 seqs, 96216763 residues
Word size: 10
Total number of hits satisfying chosen parameters: 19
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 90 summaries
Database : PIR 80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	374	100.0	374 2 I38450 chemokine (C-C) re
2	313	83.7	360 2 JC2443 chemokine (C-C) re
3	26	7.0	352 2 A43113 chemokine (C-C) re
4	22	5.9	355 2 G02436 chemokine (C-C) re
5	22	5.9	355 2 A45177 chemokine (C-C) re
6	22	5.9	355 2 I49339 macrophage inflamm
7	22	5.9	359 2 I49341 MIP-1 alpha recept
8	12	3.2	360 2 A57160 chemokine (C-C) re
9	12	3.2	360 2 JC4587 chemokine (C-C) re
10	12	3.2	383 2 S55594 G protein-coupled
11	11	2.9	341 2 S63666 platelet activatin
12	11	2.9	342 2 SI3638 platelet-activatin
13	11	2.9	354 2 I58186 probable G protein
14	10	2.7	308 2 I50241 G protein-coupled
15	10	2.7	327 2 S56162 MDCK15 protein - h
16	10	2.7	333 2 S78136 NADH2 dehydrogenas
17	10	2.7	372 2 S26667 G protein-coupled
18	10	2.7	374 2 S42628 G protein-coupled
19	10	2.7	374 2 S32785 G protein-coupled

ALIGNMENTS

RESULT 1
I38450
chemokine (C-C) receptor 2, splice form A - human
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
C;Accession: I38450
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant prot
A;Reference number: A53477; MUID:94195821; PMID:8146186
A;Accession: I38450
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <RES>
A;Cross-references: UNIPROT:P41597; UNIPARC:UPI0000043585; EMBL:U03882; NID:9472555; PID:
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane
F;44-68/Domain: transmembrane #status predicted <TM1>
F;79-99/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;244-265/Domain: transmembrane #status predicted <TM6>
F;292-309/Domain: transmembrane #status predicted <TM7>
F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;32-277,113-190/Disulfide bonds: #status predicted
Query Match 100.0%; Score 374; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLSTSRFPRTNTEGEEVTFDDYDYGAPCHKFDVKQIGAQLLPLSLVIFGFVGN 60
DB 1 MLSTSRFPRTNTEGEEVTFDDYDYGAPCHKFDVKQIGAQLLPLSLVIFGFVGN 60
QY 61 MLVVLILINCKLCLTDIYLLNLAIISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKLCLTDIYLLNLAIISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPILLITIDRYLAIHVAVFALKARTVTGVTSTVITLWVAFASVPGIIFTK 180
DB 121 HIGYFGGIFPILLITIDRYLAIHVAVFALKARTVTGVTSTVITLWVAFASVPGIIFTK 180
QY 181 CQKEDSVYCGPYFPRGWNFTIMRNILGLVLPLIMVICYSGILKTLRCNEKKRHR 240
DB 181 CQKEDSVYCGPYFPRGWNFTIMRNILGLVLPLIMVICYSGILKTLRCNEKKRHR 240
QY 241 AVRVIETIMVYFLWTPYINIVILLNTFOBFGLSNCESTSQLDOATQVTTGLTMTHCCI 300
DB 241 AVRVIETIMVYFLWTPYINIVILLNTFOBFGLSNCESTSQLDOATQVTTGLTMTHCCI 300
QY 301 NPIIYAFVGEKFRSLFHIALGCRIPALQKPVCGPGVRPGKNVKVTTQGLLDGRGKESI 360
DB 301 NPIIYAFVGEKFRSLFHIALGCRIPALQKPVCGPGVRPGKNVKVTTQGLLDGRGKESI 360
QY 361 GRAPEASLDQKEGA 374
DB 361 GRAPEASLDQKEGA 374
RESULT 2
JC2443
chemokine (C-C) receptor 2, splice form B - human
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: JC2443; I38463
R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant prot
A;Reference number: JC2443; MUID:94324942; PMID:8048929
A;Accession: JC2443
A;Molecule type: mRNA

A;Residues: 1-360 <YAM>
A;Cross-references: UNIPROT:P41597; UNIPARC:UPI000002A69C; DDBJ:D29984; NID:G531246; PID
R;Chao, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant pro
A;Reference number: A53477; MUID:94195821; PMID:8146186
A;Accession: I38463
A;Status: preliminary
A;Molecule type: mRNA
A;Cross-references: UNIPARC:UPI000002A69C; EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PI
A;Residues: 1-360 <RES>
A;Cross-references: UNIPARC:UPI000002A69C; EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PI
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
A;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran
F;43-70/Domain: transmembrane #status predicted <TM1>
F;81-100/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>
F;207-226/Domain: transmembrane #status predicted <TM5>
F;244-268/Domain: transmembrane #status predicted <TM6>
F;287-309/Domain: transmembrane #status predicted <TM7>
F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;113-190/Disulfide bonds: #status predicted

Query Match 83.7%; Score 313; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.5e-309;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEVVTTFDYDYGAPCHKFDVKQIGALLPLLYSLVIFGVGN 60
Db 1 MLSTSRFRIRNTNESGEVVTTFDYDYGAPCHKFDVKQIGALLPLLYSLVIFGVGN 60

QY 61 MLVVLILINCKLKCLFDIYLLNLAIISDLLFLITPLWHAASAANWVFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKLKCLFDIYLLNLAIISDLLFLITPLWHAASAANWVFGNAMCKLFTGLY 120

QY 121 HIGYFGGIFPIILLTDIYLAIVHAVFALKARTVFGVTVSVITLWVAFVPGIIFTK 180
Db 121 HIGYFGGIFPIILLTDIYLAIVHAVFALKARTVFGVTVSVITLWVAFVPGIIFTK 180

QY 181 CQKEDSVYVCGPFPFRGNWPFHTIMRNILGLVPLLLIMVICYSGILKTLRCNEKKRHR 240
Db 181 CQKEDSVYVCGPFPFRGNWPFHTIMRNILGLVPLLLIMVICYSGILKTLRCNEKKRHR 240

QY 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFPLGNCSTSQLDQATQVTTGLMTHCCI 300
Db 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFPLGNCSTSQLDQATQVTTGLMTHCCI 300

QY 301 NPIIYAFVGEKFR 313
Db 301 NPIIYAFVGEKFR 313

RESULT 3
A43113
chemokine (C-C) receptor 5 - human
N;Alternate names: C-C CKR-5; CCR5
C;Species: Homo sapiens (man)
C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000
A;Accession: A43113; S71808; A58832; G02653; A58833
R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A;Title: Molecular cloning and functional expression of a new human CC-chemokine recepto
A;Reference number: A43113; MUID:96241590; PMID:8639485
A;Accession: A43113
A;Molecule type: mRNA
A;Residues: 1-352 <SAM1>
A;Cross-references: UNIPARC:UPI000000D955; GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID
R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragost
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa

Nature 382, 722-725, 1996
A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of
A;Reference number: S71808; MUID:96345670; PMID:8751444
A;Accession: S71808
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 182-206; 207-230 <SAM2>
A;Cross-references: UNIPARC:UPI00001778E9; UNIPARC:UPI00001778EA
A;Accession: A58834
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-184, 'TKDSHLGAGPAAACHGHLILGNPKNSASVSK' <SAM3>
A;Cross-references: UNIPARC:UPI00001778E9; UNIPARC:UPI00001778EA; GB:X99393; NID:g152406;
A;Note: this frameshift mutation results in a non-functional receptor but confers a degra
nd may have had a selective advantage by conferring resistance to Yersinia plague infecti
R;Combadiere, C.; Aluja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rece
A;Reference number: A58832; MUID:96295970; PMID:8699119
A;Accession: A58832
A;Molecule type: mRNA
A;Residues: 1-352 <COM1>
A;Cross-references: UNIPARC:UPI000000D955; GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:
A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R;Combadiere, C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01541
A;Accession: G02653
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-89, 'L', '91-352 <COM2>
A;Cross-references: UNIPARC:UPI00001778EB; EMBL:U57840
R;Raport, C.J.; Goshing, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A;Title: Molecular cloning and functional characterization of a novel human CC chemokine
A;Reference number: A58833; MUID:96291862; PMID:8663314
A;Accession: A58833
A;Molecule type: mRNA
A;Residues: 1-352 <RAP>
A;Cross-references: UNIPARC:UPI000000D955; GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:
C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see
C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (C
C;Genetics:
A;Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CCR5; ChemR13
A;Cross-references: GDB:1230510; OMIM:601373
A;Map position: 3p21-3p21
C;Function:
A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
A;Note: probably acts to control granulocyte proliferation and differentiation
C;Superfamily: vertebrate rhodopsin
C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane
F;32-56/Domain: transmembrane #status predicted <TM1>
F;67-87/Domain: transmembrane #status predicted <TM2>
F;103-124/Domain: transmembrane #status predicted <TM3>
F;142-166/Domain: transmembrane #status predicted <TM4>
F;193-218/Domain: transmembrane #status predicted <TM5>
F;236-257/Domain: transmembrane #status predicted <TM6>
F;285-300/Domain: transmembrane #status predicted <TM7>
F;20-289,101-178/Disulfide bonds: #status predicted
F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 7.0%; Score 26; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.8e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 MVICYSGLIKTLRCNEKKRRAVR 243
Db 210 MVICYSGLIKTLRCNEKKRRAVR 235

RESULT 4

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 29, 2006, 14:01:15 ; Search time 190 Seconds
(without alignments)
864.882 Million cell updates/sec

Title: US-10-791-592-2
Perfect score: 374
Sequence: 1 MLSTSRFRFIRNTNSESSEV.....GKSGSTGRAPASLQDKEGA 374

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size: 10

Total number of hits satisfying chosen parameters: 374

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 90 summaries

Database : A Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	374	100.0	374	2 AAR79165	Aar79165 Human mon
2	374	100.0	374	4 AAG80107	Aag80107 Human CCR
3	374	100.0	374	6 ABU09083	Abu09083 Human che
4	374	100.0	374	7 ADD44861	Add44861 Human pro
5	374	100.0	374	7 ADD44865	Add44865 Human pro
6	374	100.0	374	7 ADP65146	Adp65146 Human che
7	374	100.0	374	8 ADO29221	Ado29221 Human GPC
8	374	100.0	374	8 ADQ67847	Adq67847 Human che
9	374	100.0	374	9 ADY15762	Ady15762 PRO polyp
10	374	100.0	374	9 ADY19514	Ady19514 PRO polyp
11	374	100.0	374	9 ADZ11713	Adz11713 Human che
12	374	100.0	374	9 ADZ75584	Adz75584 Human CC-
13	374	100.0	374	9 AEB22129	Aeb22129 Human che
14	374	100.0	374	9 AEB94404	Aeb94404 Human C-C
15	344	92.0	344	5 ABG92881	Abg92881 Class I r
16	344	92.0	344	6 ABU61655	Abu61655 Human mon
17	344	92.0	344	7 ADF72129	Adf72129 Human G-p
18	344	92.0	344	8 ADP86217	Adp86217 Human MCP
19	313	83.7	360	2 AAR79166	Aar79166 Human mon
20	313	83.7	360	2 AAW35833	Aaw35833 Human mon
21	313	83.7	360	4 AAG80108	Aag80108 Human CCR
22	313	83.7	360	4 AAU07614	Aau07614 Human wil
23	313	83.7	360	6 ABP97725	Abp97725 Amino aci
24	313	83.7	360	6 ABP81987	Abp81987 Human C-C

RESULT 1
AAR79165

ALIGNMENTS

360	8	ADM67225	Adm67225 Human adi
360	8	ADL82831	Adl82831 Human PRO
360	9	ADY15868	Ady15868 PRO polyp
347	7	ADF56627	Adf56627 Partial h
347	9	ADW15156	Adw15156 Human mon
360	4	AAU07613	Aau07613 Human CCR
360	4	ABBS6340	Abbs6340 Non-endog
329	4	ABA46859	Abba46859 Human MCP
329	5	ABB81055	Abb81055 Human MCP
329	8	ADR16266	Adr16266 Human MCP
83	2	AAV01249	Aav01249 Chemokine
61	4	AAU07615	Aau07615 Human alt
384	9	AEB22130	Aeb22130 Human che
373	8	ADM67224	Adm67224 Murine ad
373	8	ADO29222	Ado29222 Mouse GPC
373	8	ADP74040	Adp74040 Murine CC
42	4	AAG80052	Aag80052 Chemokine
352	2	AAW27125	Aaw27125 Macaque c
352	2	AAW07602	Aaw07602 Human G-p
352	3	AAW80128	Aaw80128 Human G-p
352	4	AAG79089	Aag79089 Amino aci
352	4	AAE07046	Aae07046 Human G-p
352	4	AAE07037	Aae07037 Human G-p
352	5	AAU97150	Aau97150 Human G-p
352	5	ABG92880	Abg92880 Human G-p
352	5	AAE25808	Aae25808 Human G-p
352	7	ADC03359	Adc03359 Macaque c
352	7	ADF72122	Adf72122 Human G-p
352	8	ADT90865	Adt90865 Macaque s
352	8	ADU47744	Adu47744 Macaque c
35	35	AAW72685	Aaw72685 Human (MC
31	2	AAR79169	Aar79169 End of th
354	8	AAW54037	Aaw54037 Mouse CC-
354	8	ADQ29228	Adq29228 Mouse GPC
354	7	ADD44859	Add44859 Rat Prote
354	7	ADD44863	Add44863 Rat Prote
28	4	AAG80080	Aag80080 Chemokine
28	2	AAW23835	Aaw23835 Human CC
28	2	AAW27123	Aaw27123 Human che
268	7	ADC10142	Adc10142 Human NOV
268	7	ADC10144	Adc10144 Human NOV
300	8	ADY27202	Ady27202 Amino aci
326	8	ADY27192	Ady27192 Amino aci
332	2	AAW26766	Aaw26766 Human che
352	2	AAW27407	Aaw27407 Human CCR
352	2	AAW23835	Aaw23835 Human CC
352	2	AAW82332	Aaw82332 HIV-1 CO-
352	4	AAE07048	Aae07048 Human G-p
352	4	AAG80111	Aag80111 Human CCR
352	4	AAE04321	Aae04321 Human che
352	4	AAE07039	Aae07039 Human G-p
352	4	ABA46858	Abba46858 Human HDG
352	4	ABBS6342	Abbs6342 Non-endog
352	4	AAE83354	Aae83354 Human CCR
352	4	AAE82948	Aae82948 Human HIV
352	5	AAU97152	Aau97152 Human G-p
352	5	AAW52829	Aaw52829 Human CCR
352	5	AAW52828	Aaw52828 Human CC
352	5	ABG70597	Abg70597 Human G-p
352	5	ABG92883	Abg92883 Human imm
352	5	AAE25811	Aae25811 Human G-p
352	5	ABB81054	Abb81054 G-protein
352	5	ABB08343	Abb08343 Human che
352	6	ABG75540	Abg75540 Human G-p
352	6	ABBS6602	Abbs6602 Human can
352	6	AAO29514	Aao29514 Human C-C

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OM protein - protein search, using sw model

Run on: March 29, 2006, 14:21:06 ; Search time 25 Seconds
(without alignments)
455.411 Million cell updates/sec

Title: US-10-791-592-2

Perfect score: 374

Sequence: 1 MLSTSRPFIRNTNESGEV.....GKGSGIGRAPEASLQDKEGA 374

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 180808 seqs, 30441898 residues

Word size: 10

Total number of hits satisfying chosen parameters: 15

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 90 summaries

Database : Published Applications AA New:

- 1: /SIDSS/ptodata/2/pubpaa/US08 NEW PUB.pap.*
- 2: /SIDSS/ptodata/2/pubpaa/US06 NEW PUB.pap.*
- 3: /SIDSS/ptodata/2/pubpaa/US07 NEW PUB.pap.*
- 4: /SIDSS/ptodata/2/pubpaa/PCT NEW PUB.pap.*
- 5: /SIDSS/ptodata/2/pubpaa/US09 NEW PUB.pap.*
- 6: /SIDSS/ptodata/2/pubpaa/US10 NEW PUB.pap.*
- 7: /SIDSS/ptodata/2/pubpaa/US11 NEW PUB.pap.*
- 8: /SIDSS/ptodata/2/pubpaa/US60 NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	374	100.0	374	7	US-11-127-877-60
2	39	10.4	352	7	US-11-068-686-20
3	26	7.0	352	6	US-10-995-561-523
4	26	7.0	352	7	US-11-068-686-2
5	26	7.0	352	7	US-11-127-877-61
6	23	6.1	216	6	US-10-995-561-522
7	22	5.9	355	7	US-11-068-686-4
8	22	5.9	355	7	US-11-127-877-64
9	22	5.9	355	7	US-11-216-610-2
10	22	5.9	355	7	US-11-216-610-4
11	22	5.9	355	7	US-11-216-610-6
12	12	3.2	360	6	US-10-959-310-36
13	12	3.2	360	7	US-11-144-731-1
14	12	3.2	360	7	US-11-262-284-34
15	10	2.7	346	7	US-11-157-930-2

ALIGNMENTS

RESULT 1
US-11-127-877-60
; Sequence 60, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:

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; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 60
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-60

Query Match      100.0%; Score 374; DB 7; Length 374;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 MLVVLILINCKKCLTDIYLLNLATSDLLFLITPLWAHSAANWVFGNAMCKLFTGLY 120
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Qy      121 HIGVFGGIFPIILLTIDRYLAIHVAHFALKARTVFGVTSVITLWVAFASVPGIIFTK 180
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Qy      181 CQKEDSVYVCGPYFPRGWNHFTIMRNILGLVLPILLIMVICYSGILKTLRCNEKKRHR 240
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Db      301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGPGVPRGKVKVVTQGLLDGRGKSI 360

Qy      361 GRAPEASLQDKEGA 374
Db      361 GRAPEASLQDKEGA 374

RESULT 2
US-11-068-686-20
; Sequence 20, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
;               Schweickart, Vicky L.
;               Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/068,686
; FILING DATE: 28-Feb-2005
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-11-068-686-20

Query Match 10.4%; Score 39; DB 7; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.1e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 115 GIPFIILLTDYLAIVHAVFALKARTVTRGVTSVITW 153

RESULT 3
US-10-995-561-523
; Sequence 523, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 523
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-523

Query Match 7.0%; Score 26; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 MVICYSGILKTLRCRNEKKRHRAVR 243
Db 210 MVICYSGILKTLRCRNEKKRHRAVR 235

RESULT 4
US-11-068-686-2
; Sequence 2, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; APPLICANT: Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

```

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;
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/068,686
; FILING DATE: 28-Feb-2005
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "98C amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-11-068-686-2

Query Match 7.0%; Score 26; DB 7; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 MVICYSGILKTLRCRNEKKRHRAVR 243
Db 210 MVICYSGILKTLRCRNEKKRHRAVR 235

RESULT 5
US-11-127-877-61
; Sequence 61, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-61

Query Match 7.0%; Score 26; DB 7; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 MVICYSGILKTLRCRNEKKRHRAVR 243

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Title: US-10-791-592-2

Perfect score: 374

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Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 10

Total number of hits satisfying chosen parameters: 335

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 90 summaries

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- 6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	374	100.0	374	3	US-09-893-512-13
2	374	100.0	374	4	US-10-039-659-14
3	374	100.0	374	4	US-10-239-423-63
4	374	100.0	374	4	US-10-754-071-14
5	374	100.0	374	4	US-10-741-601-287
6	374	100.0	374	5	US-10-791-592-2
7	374	100.0	374	5	US-10-791-166-2
8	374	100.0	374	5	US-10-759-860-14
9	374	100.0	374	5	US-10-799-736-13
10	374	100.0	374	5	US-10-988-267-2
11	374	100.0	374	5	US-10-773-446-126
12	374	100.0	374	5	US-10-287-436A-387
13	374	100.0	374	5	US-10-287-436A-1087
14	374	100.0	374	6	US-11-021-951-161
15	344	92.0	344	3	US-09-779-879A-9
16	344	92.0	344	3	US-09-779-880A-9
17	344	92.0	344	4	US-10-232-686-9
18	344	92.0	344	4	US-10-067-800-9
19	344	92.0	344	4	US-10-135-839-9
20	344	92.0	344	5	US-10-984-679-9
21	313	83.7	359	5	US-10-988-267-24
22	313	83.7	360	3	US-09-131-827A-2
23	313	83.7	360	4	US-10-225-567A-460
24	313	83.7	360	4	US-10-164-649-50
25	313	83.7	360	4	US-10-239-423-64
26	313	83.7	360	4	US-10-439-845-8
27	313	83.7	360	4	US-10-741-601-285

ALIGNMENTS

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; Sequence 13, Application US/09893512
; Publication NO. US20030017530A1
; GENERAL INFORMATION:

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29	313	83.7	360	5	US-10-791-592-4	Sequence 4, Appli
30	313	83.7	360	5	US-10-791-166-4	Sequence 4, Appli
31	313	83.7	360	5	US-10-700-313-8	Sequence 8, Appli
32	313	83.7	360	5	US-10-486-471-4	Sequence 4, Appli
33	313	83.7	360	5	US-10-846-185-8	Sequence 8, Appli
34	313	83.7	360	5	US-10-988-267-4	Sequence 4, Appli
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36	300	80.2	347	4	US-10-176-078-3	Sequence 3, Appli
37	300	80.2	347	5	US-10-893-996-3	Sequence 3, Appli
38	249	66.6	360	3	US-09-131-827A-20	Sequence 20, Appl
39	241	64.4	360	3	US-09-826-509-473	Sequence 473, App
40	241	64.4	360	5	US-10-925-095-473	Sequence 473, App
41	224	59.9	329	3	US-09-725-285-9	Sequence 9, Appli
42	224	59.9	329	3	US-09-195-662A-9	Sequence 9, Appli
43	224	59.9	329	3	US-09-339-912A-9	Sequence 9, Appli
44	224	59.9	329	3	US-09-502-783A-9	Sequence 9, Appli
45	224	59.9	329	4	US-10-791-905-9	Sequence 9, Appli
46	224	59.9	329	5	US-10-127-764-9	Sequence 7, Appli
47	194	51.9	360	3	US-09-938-719-7	Sequence 7, Appli
48	194	51.9	360	3	US-09-939-226-7	Sequence 7, Appli
49	194	51.9	360	3	US-09-938-703-7	Sequence 7, Appli
50	194	51.9	360	4	US-10-661-798-7	Sequence 7, Appli
51	194	51.9	360	4	US-10-612-791-7	Sequence 7, Appli
52	83	22.2	83	3	US-09-131-827A-13	Sequence 13, Appl
53	59	15.8	360	4	US-10-164-649-51	Sequence 51, Appl
54	50	13.4	384	3	US-09-893-512-14	Sequence 14, Appl
55	50	13.4	384	5	US-10-799-736-14	Sequence 14, Appl
56	42	11.2	42	4	US-10-239-423-8	Sequence 8, Appli
57	39	10.4	352	3	US-09-779-879A-2	Sequence 2, Appli
58	39	10.4	352	3	US-09-779-880A-2	Sequence 2, Appli
59	39	10.4	352	4	US-10-106-623-20	Sequence 20, Appl
60	39	10.4	352	4	US-10-151-274-5	Sequence 5, Appli
61	39	10.4	352	4	US-10-067-800-2	Sequence 2, Appli
62	39	10.4	352	4	US-10-164-649-52	Sequence 52, Appli
63	39	10.4	352	4	US-10-135-839-2	Sequence 2, Appli
64	39	10.4	352	5	US-10-772-037-20	Sequence 20, Appl
65	39	10.4	352	5	US-10-594-679-2	Sequence 2, Appli
66	35	9.4	35	4	US-10-082-815-6	Sequence 6, Appli
67	35	9.4	35	5	US-10-983-453-6	Sequence 6, Appli
68	31	8.3	31	5	US-10-791-592-13	Sequence 13, Appl
69	31	8.3	31	5	US-10-791-166-13	Sequence 13, Appl
70	28	7.5	28	4	US-10-239-423-36	Sequence 36, Appl
71	26	7.0	332	4	US-10-095-876A-2	Sequence 2, Appli
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73	26	7.0	332	3	US-09-759-841-2	Sequence 2, Appli
74	26	7.0	332	3	US-09-779-879A-22	Sequence 22, Appl
75	26	7.0	332	3	US-09-779-880A-22	Sequence 22, Appl
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79	26	7.0	332	3	US-09-195-662A-2	Sequence 2, Appli
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85	26	7.0	332	3	US-09-734-221A-14	Sequence 14, Appl
86	26	7.0	332	3	US-09-826-509-477	Sequence 477, App
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89	26	7.0	332	4	US-10-086-814-1	Sequence 1, Appli
90	26	7.0	332	4	US-10-067-800-22	Sequence 22, Appl

APPLICANT: OWMAN, CHRISTER
TITLE OF INVENTION: HEPTAHELIX RECEPTOR AND ITS USE AS LEUKOTRIENE B4
FILE REFERENCE: 07675.0001-03 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/09/893,512
CURRENT FILING DATE: 2001-06-29
PRIOR FILING DATE: 1997-10-14
PRIOR APPLICATION NUMBER: 60/061,789
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081,958
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 09/170,069
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 374
TYPE: PRT
ORGANISM: Homo sapiens
US-09-893-512-13

Query Match 100.0%; Score 374; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGVGN 60
QY 61 MLVVLILINCKKLCITDIYLLNLAIISDLLFLITPLWHAHSAANWVFGNAMCKLFTGLY 120
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QY 121 HIGYFGGIFPIILLTIDRYLAIHVAFAKARTVTFGVVTSVITLWVAFASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTIDRYLAIHVAFAKARTVTFGVVTSVITLWVAFASVPGIIFTK 180
QY 181 CQKEDSVVYCGPYFPRGWNFNHTIMRNILGLVPLLIWVICYSGILKTLRCRNEKKRHR 240
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QY 241 AVRVIPTIMIVFLFWTPYNNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCI 300
DB 241 AVRVIPTIMIVFLFWTPYNNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCI 300
QY 301 NPIIYAFVGEKFRSLFHIALGCRITAPLOKPCGPGVVRPGKNVKVTTQGLLDGRGKXSI 360
DB 301 NPIIYAFVGEKFRSLFHIALGCRITAPLOKPCGPGVVRPGKNVKVTTQGLLDGRGKXSI 360
QY 361 GRAPEASLQDKEGA 374
DB 361 GRAPEASLQDKEGA 374

RESULT 2
US-10-039-659-14
Sequence 14, Application US/10039659
Publication No. US20030018167A1
GENERAL INFORMATION:
APPLICANT: Wang, Wei
Gish, Kurt C.
Schall, Thomas J.
Vicari, Alain P.
Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/039,659
FILING DATE: 03-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/887,977
FILING DATE: 03-JUL-1997
APPLICATION NUMBER: US 60/021,644
FILING DATE: 05-JUL-1996
APPLICATION NUMBER: US 60/028,329
FILING DATE: 11-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0589K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9192
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-039-659-14

Query Match 100.0%; Score 374; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGVGN 60
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QY 361 GRAPEASLQDKEGA 374
DB 361 GRAPEASLQDKEGA 374

RESULT 3
US-10-239-423-63
Sequence 63, Application US/10239423
Publication No. US20030186889A1
GENERAL INFORMATION:
APPLICANT: FORSMANN, Wolf-Georg; FORSMANN, Ulf; ADERMAN, Knut;
APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikola
TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the

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OM protein - protein search, using sw model

Run on: March 29, 2006, 14:08:45 ; Search time 46 Seconds
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672.189 Million cell updates/sec

Title: US-10-791-592-2
Perfect score: 374
Sequence: 1 MLTSRFRFRNTNESGEEV.....GKGSGTGRAPEASLDQKGA 374

Scoring table: OMIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size: 8

Total number of hits satisfying chosen parameters: 154

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 90 summaries

- Database : Issued Patents AA.*
1: /cgm2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgm2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgm2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgm2_6/ptodata/1/iaa/PCTUS COMB.pep.*
5: /cgm2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	374	100.0	374	1	US-08-450-393A-2
2	374	100.0	374	2	US-08-446-669-2
3	374	100.0	374	2	US-10-039-659A-14
4	374	100.0	374	2	US-09-625-573-2
5	374	100.0	374	4	PCT-US95-00476-2
6	374	100.0	387	2	US-09-949-016-11222
7	344	92.0	344	2	US-08-466-343D-9
8	344	92.0	344	2	US-09-502-784A-9
9	313	83.7	360	1	US-08-450-393A-4
10	313	83.7	360	2	US-08-446-669-4
11	313	83.7	360	2	US-09-045-583-50
12	313	83.7	360	2	US-09-534-185-50
13	313	83.7	360	2	US-09-131-827A-2
14	313	83.7	360	2	US-09-625-573-4
15	313	83.7	360	4	PCT-US95-00476-4
16	313	83.7	377	2	US-09-949-016-11221
17	300	80.2	347	1	US-08-461-244-3
18	249	66.6	360	2	US-09-131-827A-20
19	241	64.4	360	2	US-09-826-509-473
20	224	59.9	329	2	US-09-502-783A-9
21	224	59.9	329	2	US-09-339-912A-9
22	224	59.9	329	2	US-09-195-662A-9
23	194	51.9	360	2	US-08-833-752-7
24	194	51.9	360	2	US-09-938-719-7
25	194	51.9	360	2	US-09-939-226B-7
26	194	51.9	360	2	US-09-938-703B-7
27	83	22.2	83	2	US-09-131-827A-13

ALIGNMENTS

RESULT 1
US-08-450-393A-2
; Sequence 2, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:

28	59	15.8	360	2	US-09-045-583-51	Sequence 51, Appl
29	59	15.8	360	2	US-09-534-185-51	Sequence 51, Appl
30	39	10.4	352	2	US-08-466-343D-2	Sequence 2, Appl
31	39	10.4	352	2	US-09-045-583-52	Sequence 52, Appl
32	39	10.4	352	2	US-09-517-605-5	Sequence 5, Appl
33	39	10.4	352	2	US-09-534-185-52	Sequence 52, Appl
34	39	10.4	352	2	US-08-771-276-20	Sequence 20, Appl
35	31	8.3	351	1	US-08-450-393A-13	Sequence 13, Appl
36	31	8.3	351	2	US-08-446-669-13	Sequence 13, Appl
37	31	8.3	351	2	US-09-625-573-13	Sequence 13, Appl
38	31	8.3	354	4	PCT-US95-00476-13	Sequence 2, Appl
39	31	8.3	354	2	US-08-724-984A-2	Sequence 2, Appl
40	26	7.0	352	2	US-09-087-232A-13	Sequence 13, Appl
41	26	7.0	352	2	US-08-861-105-14	Sequence 14, Appl
42	26	7.0	352	2	US-08-575-967A-2	Sequence 2, Appl
43	26	7.0	352	2	US-08-833-752-5	Sequence 5, Appl
44	26	7.0	352	2	US-09-502-783A-2	Sequence 2, Appl
45	26	7.0	352	2	US-09-796-202-1	Sequence 1, Appl
46	26	7.0	352	2	US-09-938-719-5	Sequence 5, Appl
47	26	7.0	352	2	US-09-502-784A-2	Sequence 2, Appl
48	26	7.0	352	2	US-09-339-912A-2	Sequence 2, Appl
49	26	7.0	352	2	US-08-771-276-2	Sequence 2, Appl
50	26	7.0	352	2	US-09-939-226B-5	Sequence 5, Appl
51	26	7.0	352	2	US-09-195-662A-2	Sequence 2, Appl
52	26	7.0	352	2	US-09-826-509-477	Sequence 477, App
53	26	7.0	352	2	US-09-949-002-303	Sequence 303, App
54	26	7.0	352	2	US-10-323-314-1	Sequence 1, Appl
55	26	7.0	352	2	US-09-938-703B-5	Sequence 5, Appl
56	26	7.0	378	2	US-09-949-002-552	Sequence 552, App
57	23	6.1	184	2	US-08-833-752-4	Sequence 4, Appl
58	23	6.1	184	2	US-09-938-719-4	Sequence 4, Appl
59	23	6.1	184	2	US-09-939-226B-4	Sequence 4, Appl
60	23	6.1	184	2	US-09-938-703B-4	Sequence 4, Appl
61	23	6.1	215	2	US-09-087-232A-17	Sequence 17, Appl
62	23	6.1	215	2	US-08-833-752-6	Sequence 6, Appl
63	23	6.1	215	2	US-09-938-719-6	Sequence 6, Appl
64	23	6.1	215	2	US-09-939-226B-6	Sequence 6, Appl
65	23	6.1	215	2	US-09-939-226B-18	Sequence 18, Appl
66	23	6.1	215	2	US-09-938-703B-6	Sequence 6, Appl
67	23	6.1	215	2	US-09-938-703B-18	Sequence 18, Appl
68	22	5.9	27	2	US-09-087-232A-23	Sequence 23, Appl
69	22	5.9	31	1	US-08-450-393A-14	Sequence 14, Appl
70	22	5.9	31	2	US-08-446-669-14	Sequence 14, Appl
71	22	5.9	31	2	US-09-625-573-14	Sequence 14, Appl
72	22	5.9	31	4	PCT-US95-00476-14	Sequence 2, Appl
73	22	5.9	355	1	US-08-012-988A-2	Sequence 2, Appl
74	22	5.9	355	1	US-08-450-393A-5	Sequence 5, Appl
75	22	5.9	355	2	US-08-446-669-5	Sequence 5, Appl
76	22	5.9	355	2	US-08-575-967A-4	Sequence 4, Appl
77	22	5.9	355	2	US-08-847-296B-1	Sequence 1, Appl
78	22	5.9	355	2	US-09-045-583-53	Sequence 53, Appl
79	22	5.9	355	2	US-09-045-583-54	Sequence 54, Appl
80	22	5.9	355	2	US-09-239-938-1	Sequence 1, Appl
81	22	5.9	355	2	US-09-534-185-53	Sequence 53, Appl
82	22	5.9	355	2	US-09-534-185-54	Sequence 54, Appl
83	22	5.9	355	2	US-08-720-565-2	Sequence 2, Appl
84	22	5.9	355	2	US-08-720-565-4	Sequence 4, Appl
85	22	5.9	355	2	US-08-720-565-6	Sequence 6, Appl
86	22	5.9	355	2	US-09-886-319A-13	Sequence 13, Appl
87	22	5.9	355	2	US-09-886-319A-14	Sequence 14, Appl
88	22	5.9	355	2	US-09-931-381A-16	Sequence 16, Appl
89	22	5.9	355	2	US-10-039-659A-13	Sequence 13, Appl
90	22	5.9	355	2	US-10-039-659A-15	Sequence 15, Appl

APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Coolley Godward Castro Huddleson & Tatum
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cseri, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
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TELEFAX: 415-8857-0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-393A-2

Query Match 100.0%; Score 374; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLSTSRSRFIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGVGN 60
Db 1 MLSTSRSRFIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGVGN 60
Qy 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120
Qy 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180
Db 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180
Qy 181 CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240
Db 181 CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240
Qy 241 AVRVIPTIMIVYFLFWTPYNNVILLNTFQBFPGLSNCESTSQLDQATQVTTETLGMTHCCI 300
Db 241 AVRVIPTIMIVYFLFWTPYNNVILLNTFQBFPGLSNCESTSQLDQATQVTTETLGMTHCCI 300
Qy 301 NPIIYAFVGEKFSRSLFHIALGCRIPAPLQKPGVCGGPGVRPGKNVKTQGLLDGRGKSI 360
Db 301 NPIIYAFVGEKFSRSLFHIALGCRIPAPLQKPGVCGGPGVRPGKNVKTQGLLDGRGKSI 360
Qy 361 GRAPEASLQDKEGA 374
Db 361 GRAPEASLQDKEGA 374

RESULT 2
US-08-446-669-2
; Sequence 2, Application US/08446669

Patent No. 6132987
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Coolley Godward Castro Huddleson & Tatum
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELECOMMUNICATION INFORMATION:
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TELEFAX: 415-857-0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-669-2

Query Match 100.0%; Score 374; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLSTSRSRFIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGVGN 60
Db 1 MLSTSRSRFIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGVGN 60
Qy 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120
Qy 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180
Db 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180
Qy 181 CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240
Db 181 CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240
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Db 241 AVRVIPTIMIVYFLFWTPYNNVILLNTFQBFPGLSNCESTSQLDQATQVTTETLGMTHCCI 300
Qy 301 NPIIYAFVGEKFSRSLFHIALGCRIPAPLQKPGVCGGPGVRPGKNVKTQGLLDGRGKSI 360
Db 301 NPIIYAFVGEKFSRSLFHIALGCRIPAPLQKPGVCGGPGVRPGKNVKTQGLLDGRGKSI 360
Qy 361 GRAPEASLQDKEGA 374
Db 361 GRAPEASLQDKEGA 374

RESULT 3